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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

August 3, 2005, 17:11:04; Search time 7197 Seconds (without alignments) 11847.153 Million cell updates/sec Run on:

Title: Perfect score:

Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

34239544 segs, 19032134700 residues Searched:

159776 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 50

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

gb\_est1:; gb\_htc:; gb\_est3:; gb\_est4:; gb\_est6:; gb\_gs81:; gb\_gs81:; EST:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## CTIMMADITE

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
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Ŋ	36	1.6	20	Н	AU104985	AU104985 AU104985
g	34.4	1.5	20	Н	AU104974	AU104974 AU104974
7	34.4	1.5	20	Н	AU104977	AU104977 AU104977
œ	34.4	1.5	20	-	AU104980	AU104980 AU104980
σ	34	1.5	20	٦	AU104976	AU104976 AU104976
0	33.8	1.5	37	œ	AZ761912	AZ761912 1M0556D02
-	33	1.5	20	-	AU104983	AU104983 AU104983
~	32.2	1.4	45	8	AZ843544	AZ843544 2M0142022
e,	32	1.4	20	Н	AU104984	AU104984 AU104984
4	32	1.4	20	Н	AU104986	AU104986 AU104986
ស	30.8	1.4	20	σ	BX976589	BX976589 Forward s
9	30.2	1.3	43	œ	AZ419099	AZ419099 1M0195N23
17	29.6	1.3	37	60	AZ392980	AZ392980 1M0155P13
81	29.6	1.3	37	60	AZ623276	AZ623276 1M0460M16
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21	29.2	1.3	20	٦	AI252059	AI252059 qv39f04.x
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CG731182 1119136A0 AZ792853 2M0045C07 AU103294 AU103294 AZ455186 1M022E03		DFLU/886 001823895 AA145482 mr62806.r AA590944 vm25f02.r aza68544 om0246120		AZ358097 1M0100N08 AZ816605 2M0085K24 AZ861629 2M0168A19	
CG731182 AZ792853 AU103294 AZ435186	CD577044 CR430378 AZ627160	BF10/886 AA145482 AA590944 AA5968544	AZ407440 BI491464 CV304274	AZ358097 AZ816605 AZ861629	AZ967786 CR003825 CR048038
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## ALIGNMENTS

	National Cander Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)  Contact: Robert Strausberg, Ph.D. Contact: Robert Strausberg, Ph.D. Email: Gapba-remail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Stratagene, Inc., David B. Krizman, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. CDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NGT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html	Trace considered overall poor quality Insert Length: 1604 Std Brror: 0.00 Seq primer: -40ml3 Hwd. BT from Amersham High quality sequence stop: 1. Location/Qualifiers 1. 46
RESULT 1 AA995439/c LOCUS DEFINITION ACCESSION VERYORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL COMMENT	FEATURES SOURCE

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Department of Virology
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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8mail: ysuzuki@ims.u-cokyo.ac.jp
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Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
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1 (Dassel to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="CASO8333"
/clone_lib="Sugano Homo sapiens cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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AU104981
AU104981.1 GI:13554502
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nes 36; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 50)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Diverse transcriptional initiation revealed by fine, large-scale
                                                                                                      Gaps
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Pred. No. 2e+02;
0; Mismatches 2; Indels
                                                                                                                                                   1060 TATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGA 1104
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                                                                                                                                                                              45 TATTAACCTATGTTGGTGCCTTGTTTATTGGTCTGACACTACTGA 1
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EMBO Rep. 2 (5), 388-393 (2001)
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Best Local Similarity 100.
Matches 36; Conservative
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                                               Query Match
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Matches 43; Conserv
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Institute of Medical Science, University of Tokyo
Suzuki, Mirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
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Sugano,S. Construction and characterization of a full
Inength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Secondary, Marokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Yr. Yoshitomo-Nakagawa,Kr. Maruyama,Kr. Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 50.)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Bakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
  Diverse transcriptional initiation revealed by fine, large-scale
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/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 50;
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Pred. No. 8.8e+03;
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Pred. No. 8.8e+03;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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21270072
                  mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
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Best Local Similarity 97.2%;
Matches 35; Conservative
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ima.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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(Dases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 50)

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Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/mol_type="mRNA"
/db_xref="txxon:9606"
/db_xref="HX101927"
/clone_lib="Sugano Homo sapiens cDNA library"
1.6%; Score 36; DB 1; Length 50;
100.0%; Pred. No. 3.9e+03;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.9e+03;
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                             Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nede, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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1M0555D02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0555D02 R, genomic survey sequence.
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CA902067"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                            Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
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100.0%; Pred. No. 1.1e+04;
ive 0; Mismatches 0; Indels
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Seg primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
/strain="C57BL/6J"
    Rep. 2 (5), 388-393 (2001)
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Insert Length: 10000 Std Erro
Plate: 0556 row: D column: 02
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Mus musculus
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                                                                      Contact: Yutaka Suzuki
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Best Local Similarity 100.0
Matches 34; Conservative
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Fax: 801 585 7177
Email: ddunn@genet
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Suzuki, Mirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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1 (Dases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Bata,H., Ota,T., 1sogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 50)
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Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
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/db_xref="taxon:9606"
/clone="COL10301"
/clone_lib="Sugano Homo sapiens cDNA library"
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                                              1 CGTCACCACAGTAGGTCCCTCGGCTCAGTCGGCCCA 36
                                                                           15 CGTGACCACAGTAGGTCCCTCGGCTCAGTCGGCCCA 50
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    0; Mismatches
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    35; Conservative
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KEYWORDS
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AU104976
LOCUS
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KEYWORDS
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Laboratory Mouse DNA Resource Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (Jases 1 to 45)
Eu (Jases 1 t
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                                                                                                                                                                                                                                                                                            GSS 20-FEB-2001
                                                                                                                                                                                                                                                                                        AZ843544 1inear GSS 20-FEB-200
2M0142022F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0142022 F, genomic survey sequence.
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/clone lib="Mouse 10kb plasmid UUGCNM library."
/note="Vector: PWD4ZNY; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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1.4%; Score 32.2; DB 8; Length 45;
Best Local Similarity 91.9%; Pred. No. 2.6e+04;
Matches 34; Conservative 0; Mismatches 3; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0142 row: O column: 22
Seg primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends
                    37
                                                                                     50
                    5 ACCACAGIAGGICCCICGGCICAGICGGCCCAG
                                                                 18 ACCACAGTAGGTCCCTCGGCTCAGTCGGCCCAG
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/mol_type="genomic DNA"
strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC2M0142022"
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Location/Qualifiers
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AZ843544.1 GI:13013452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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AZ843544/c
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Labocratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil 4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,R., Maruyama,R., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2),
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
ENERG Rep. 2 (5), 388-393 (2001)
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/db_xref="taxon:9606"
/clone="HRC11726"
/clone_lib="Sugano Homo sapiens cDNA library"
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100.0%; Pred. No. 1.8e+04;
ive 0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 33; Conservative
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BX976589
BX976589.1 GI:49708012
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Best Local Similarity 100.
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Best Local Similarity
Matches 38; Conserv
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BX976589/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Yr. Yoshitomo-Nakagawa,Kr. Maruyama,Kr. Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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                                                                                                                                      AU104984 50 amrNA linear EST 28-JAN-2004 AU104984 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC11752, mRNA sequence.
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 50)

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Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S., Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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Hata,H., Ota,T., 1sogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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100.0%; Pred. No. 3e+04;
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237 GAGGAGGAGGAGGAGGAGGAGGAGGACGAGG 273
                        GAGGAGGAGGAGGAGGAGGAAGAAGAGGAGGAGG
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Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugamo,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Brect Submission
Submitted (20-FRB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
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Mus musculus (house mouse)
Mus musculus
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Run on:

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BC012619 Homo sapi
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BC068991 Homo sapi
ARD40645 Homo sapi
AF132047 Homo sapi
AF132047 Homo sapi
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CQ769577 Sequence
BD12437 Homo sapi
CQ783030 Sequence
BD12437 Primer fo
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cc c12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
G01N33/566//
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BD24946 Protein B
AJ251381 Homo sapi
CQ829486 Sequence
AX195249 Sequence
AB020693 Homo sapi
AB040462 Homo sapi
AF145537 Homo sapi
CQ870070 Secreted
AX102279 Homo sapi
BD270070 Secreted
AX220865 Sequence
AX766046 Sequence
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PF 21-JUL-1999 JP 2000561310
PR 22-JUL-1998 GB 9816024.5,19-JUL-1999 GB
DAVID MICHALOVICH, RABINDER KUMAR PRINJHA
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AUTHORS
TITLE
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AJ251384 Homo sapi
BC010737 Homo sapi
BD231889 Bone marr
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                     OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                  of hits satisfying chosen parameters:
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Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext
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Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline
Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
      GTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCT
                                                                                                   841 AACTGCACGATAAAGGAACTCAGCGCCTCTTCTTAGTTGATGATGTTAGTTGATTCTCTG
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                                                                    GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal
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Christele,G., Michalovich,D., Simmons,D.L. and Walsh,F.S.
Inhibitor of neurite outgrowth in humans
Nature 403 (6768), 383-384 (2000)
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protein (Nogo gene).
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/mol type="mRNA"
/db_xref="taxon:9606"
1. .1122
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Homo sapiens (human)
Homo sapiens
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Michalovich, D.
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/organism="Homo sapiens"
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8	gnment Scores:  4. No.:  1.879.00  1.879.00  1.879.00  2.97e-67  2.98.20  2.98.30  2.98.30  2.98.30  2.98.30  2.98.30  2.98.30  2.99.544-776-2 (1-373) x HSA251384 (1-1122)  2.99-544-776-2 (1-373) x HSA251384 (1-1122)	ATGGARIACCTIGGACCAGTCTCCTCTGGTCTCGTCCTCGGACGCCCCACCCCGGCCGCGGCGCGGCGGGCG	GluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla	GCCGGGCTCCCCCCACCCCCCCCCCCCCCCGCCCCCCCCC	AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro	SerPheLeuSerAlaAlaAlaValSerFroSerLysLeuProGluAspAspGluProPro	AlaargProProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 	ProProAlaProAlaProAlaAlaProBroSerThrProAlaAlaProLysArgArgGly	SerSerGlySerValValValAspLeuLeuTyrTrpArgAspIleLysThrGlyVal 	ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal 	ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGly	41 ValileginalaileginiyaSeraspgiugiyHisProPheArgAlaTyrLeugluSer 	61 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 	ABNCYSThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 	LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr

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Entaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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16-APP-2002511231-A/3
16-APP-2002511231-A/3
16-APP-2002511231-A/3
16-APP-2002511231-A/3
16-APP-2002511231-A/3
18-DEC-1998 US 60/102540
HAISHAN LIN.LI CAO
CI2N15/09,A61K38/00,A61P43/00,C07K14/47,C07K16/18,C12N5/10,
                       ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal
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Bone marrow secreted proteins and polynucleotides.
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JP 2002511231-A/3.
Homo sapiens (human)
Homo sapiens
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VYTATLALLISVTISFRIYGVIQAA CKSBGEHPRAYLESEVAISEELVÖKYSNSA
LGHYNCTIKELRRLELDUDIVDSLKRAYLAWYFTYGALFNGLTLLILALISLFSVPV
IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
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                 analysis
This clone has the following problem: The cds is short compared
the longest cds in the locus.
Location/Qualifiers
1. 1485
/organism="Homo sapiens"
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                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="INAGE:390133"
/tissue type="Pancreas, epithelioid carcinoma"
/clone lib="with MGC_70"
/lab host="bH10B"
/note="Vector: pCMV-SPORT6"
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Matches:
Conservative:
Mismatches:
Indels:
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/product="reticulon 4, isoform
/protein id="AAH10737.1"
/db_xreff="GI:14789601".
                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="RTN4"
/note="synonyms: NSP-CL, N/db xref="LocusID:57142"
/db xref="LocusID:57142"
6. 1127
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Best Local Similarity:
Query Match:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1668)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubhin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.B.,
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Homo sapiens reticulon 4, transcript variant 2, mRNA (cDNA clone
IMAGE:3862911), complete cds.
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                                                                                                                                                                                                                                                                                                                             ValileGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer
                                                                                                                                                    ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal
                                                                                                                                                                             GTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTA
                                                                                                                                                                                                                                         221 ThralaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGly
                                                                                                                                                                                                                                                                816 ACAGCCTACATTGCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGATATACAAGGT
                                                                                                                                                                                                                                                                                                                                                             876 GIGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCT
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                                                                  SerSerGlySerValValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal
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/ codon_grart=1

/ product="reticulon 4, isoform B"

/ protein id="AAN12619.1"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPAPAPAAPPSTPAAPKREGSSGSVVVDLLYWRDIKKTGVVFGASLFLLLSTTVFSIV
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Matches:
Conservative:
Mismatches:
Indels:
  organism="Homo sapiens"
                                                                                                                                                    /note="Vector: pDNR-LIB"
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Best Local Similarity:
Query Match:
DB:
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LeuLeulleLeuAlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGln 340
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                                                                                                                ATGGAAGACCTGGACCAGTCTCCTCTGGTCTCGTCCTCGGACAGCCCACCCCGGCCGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    907 GTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAAATCT
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                                                                                                                                                                                                                      GluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla
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                                                                                                                                                                                                                                                                                                                  GCCGGGCTGTCCGCGGCCCCAGTGCCCACACGCCCCTGCCGCCGGCGGCGCCCCTGATGGAC
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         Gaps:
                                         US-09-544-776-2 (1-373) x BC026788 (1-1668)
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein
This clone has the following problem: The cds is short compared to the longest cds in the locus.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="Locueld: 57142"

/db_xref="Locueld: 57142"

/db_xref="Induceded: 57142"

/db_xref="MEDLDQSPLVSSSDSPPRQPAFKYQEVREPEDEBEEEEEEED

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PSPAPAAAPAPETPAAPKRSSSGSVVVDLLYWRDIKKTGVPGASLELLLSLTVFSIV

SVTAYIALALLSVTISFRIYKGVIQAIQASDGAPPRAALESEVAISEELLOSTYFSIV

SVTAYIALALLSVTISFRIYKGVIQAIQAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="synonyms: NSP-CL, NOGO, ASY, NI220/250, NSP, RTN-X"
                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowie, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                            Strausberg, R. Direct Submission Submission Submission Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Oby: Baylor College of Medicine Human Genome
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/tissue type="fovary, adenocarcinoma"
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/gene="RTN4"
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                                                                                                      365 GAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAGGAAGCCCGCC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160
CCCGCGTTCAAGTACCAGTTCGTGAGGGACCCGAGGACGAGGAAGAAGAAGAAGAGGAGGAG 364
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                                                                         GluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla
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IGHYNCTIKELRNLELVDDLVDSLKRAYLWWYBTPFRAYLESBYAISEELVQKYSNSA
YFRHQAQIDHYLGLANKVXDAMAKIQAKIDAKIRE"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (22-MAR-2000) Yutaka Eguchi, Osaka University Graduate School of Medicine, Biomedical Research Center, Department of Medical Genetics; Yamadaoka 2-2, Suita, Osaka 567-0871, Japan (E-mail:eguchi@gene.med.osaka-u.ac.jp, Tel:+81-6-6879-3363)
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Eguchi,Y., Tagami,S.-and Tsujimoto,Y.
Direct Submission.
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/db_xref="taxon:9606"
/tissue_type="brain"
/tissue_lib="human fetal by
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/db_xref="G1:11610577"
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Homo sapiens mRNA for RTN-xS,
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/gene="RTN-x"
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Homo sapiens
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note="synonyms: NSP-CL, NOGO, ASY, NI220/250, NSP, RIN-X" db_xref="LocusID:57142" db_xref="MIM:604475"
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SVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA
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I YERHQAQI DHYLGLANKNVKDAMAKI QAKI PGLKRKAE"
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Matches:
Conservative:
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                                                 'note="Vector: pOTB7"
                             lab host="DH10B-R"
                                                                                               gene="RTN4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.52e-67
1879.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheafer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M., B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Abramson, R.D., Mullahy, S.J., Bodsak, S.A., McEwant, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Halton, E., Ketteman, M., Madan, A., Kodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiNL at: http://image.llnl.gov Series: IRAL Plate: 54 Row: c Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28557782
This clone has the following problem: The cds is short compared to the longest cds in the locus.

Location/Qualifiers
1728 bp mRNA linear PRI 30-JUN-2004
Homo sapiens reticulon 4, transcript variant 2, mRNA (cDNA clone
MRAGE:4634289), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Buane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (05-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Conteact: MGC help desk
Email: cgapbs.f@mail.nih.gov
Tisaue Procurement: ATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="Eye, retinoblastoma"
/clone_lib="NIH_MGC_16"
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/db_xref="taxon:9606"
/clone="IMAGE:4634289"
                                                                                                                      BC068991.1 GI:46362518
                                                                                                                                                                    Homo sapiens (human)
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                                                                                                                                                                                               Homo sapiens
                                                                                               BC068991
                                                                                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                 DEFINITION
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AUTHORS
TITLE
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                                                                                           ACCESSION
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                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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BRQPSWDPSPVSSTVPARSPSPLSAAN'SPSKLPEDDEPPARPPPPPRSVSPQAEPWT
PPAPAPAPAPSPAAPKREGSSGSVVVDLYWRDIKKTGVVFGASLFLLLSLTVFSIV
SVTAYTALALLSVTJERILKYTJQJQAJQKSDEGHPFRAYLESEVAJESELVQXKSNSA
LGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLIALISLFSVPV
1YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal
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370
0
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                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                   5.81e-67
1879.00
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Best Local Similarity:
Query Match:
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                                                                               polyA_signal
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ORIGIN
                                                                                                                                      Alignment Scores:
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1 (Jases 1 to 223).
Yang, J., Yu, L., 21, A.D. and Zhao, S.Y.
Assignment of the human reticulon 4 gene (RTN4) to chromosome Cytogenet of the Applaition hybrid mapping
Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
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                                                                  AAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACA
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               ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerlleValSerVal
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Homo sapiens reticulon 4b mRNA, complete cds.
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AF148538.1 GI:10039552
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2 (bases 1 to 2235)
Zhou,Y., Yu,L. and Zhao,S.Y.
Direct Submission
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                                                              AACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTG 1041
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1 (Dases 1 to 2276)
1 (Dases 1 to 2276)
1 (Lo, T. and Schwartz, S.M.
Cloning of a member of the reticulon gene family in human: Unpublished
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GAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTG
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Homo sapiens foocen-m mRNA, complete
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Ito,T and Schwartz,S.M.

Direct Submission

Submitted (27-FEB-1999) Pathology, Un

Pacific NE, Seattle, WA 98195, USA

Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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PPAAAPPSTPAAPKRGSSGSVVVDLLVWRDLIKWTVTGVVGASLELLSLTVFSIV
IGHNVTTIKELRELSVISPRIYKGVIQAIQKSDEGHPFRAYLESEVALSEELVQKYSNSA
LGHNVATIKELRELNVDLVDSLKFAVLMWVFTYVGALFNGLTLILALISLFSVPV
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/gene="RTN4"
                                                                                              bp mRNA linear PRI 23-SEP-2003 (RTN4) mRNA, complete cds;
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J. Mol. Biol. 325 (2), 299-323 (2003)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Direct Submission
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Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
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/note="synonym: NOGO"
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Direct Submission
Sugano, S. and Suzuki, Y.
Direct Submission

1265 GCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAA 1324
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                              1525 bp mRNA linear
Homo sapiens cDNA FLJ27302 fis, clone TMS04776.
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Matches:
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oligo capping; fis (full insert sequence)
Homo sapiens (human)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TMS04776"
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/clone_lib="TMS"
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Catarrhini; Hominidae; Homo.
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261 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal
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/db_xref="GI:5821140"
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Mammalia; Butheria; Primates;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Patent: WO 200358021-A 303 17-JUL-2003
Xantos Biomedicine AG (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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     CQ769577.1 GI:45113880
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DB:
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No.:
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US-09-544	4-776-2 (1-373)	x AB015639 (1-	2052)		
Sp. GS	1 MetGluAsp          67 ATGGAAGAC	oLeuAspGlnSerPro 	LeuvalSerSerSer/ 	MetGluAspLeuAspGluSerProLeuValSerSerSerAspSerProProArgProGln 20 	
oy Oy	21 ProAlaPhe          127 CCCGCGTTC	elystyrglnPheval 	ArggluProgluAsp( 	ProblaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGluGlu 40 	
cy ea	41 GluGluGlu          187 GAAGAGGAG	JASPG1uASPG1uASP 	LeuGluGluLeuGlu\ 	GludludluaspGluaspGluaspLeuGluGluLeuGluValLeuGluargLysProala 60 	
o da	61 AlaglyLeu           247 GCCGGGCTG	SerAlaAlaProVal 	ProThrAlaProAla/ 	AlaglyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80 	
දු දු	81 PheGlyAsn          307 TTCGGAAAT	AspPheValProPro	AlaProArgGlyPheI               GGCCCGGGGACCCC	PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal 100 	
δ	101 AlaProGlu	ArgGlnProSerTrp	AspProSerProValS	-	
Dþ	367 GCCCCGGAG	SCGCCAGCCGTGTTGG	GACCCGAGCCCGGTGT	GCCCCGGAGCGGCAGCCGTGTTGGGACCCGGGGTGTCGTCGACGTGCCCGCGCCA 426	
දු පු	121 SerPheLeu     427 TCCCCGCTG	Seralaalaalava  	SerProSerLysLeuF                  TCGCCCTCCAAGCTCC	LeuSeralaalaalavalSerProSerLysLeuProGludapAspGluProPro 140 	
à t	41	ProProProPro	AlaSerValSerProC	9	
8 8		ProAlaProAlaAla	ProProSerThrPro	Arschardelleisischer 546 AlaAlaProLysArgArgGly 180	
ΩÞ	547 CCGCCAGCC		CCCCCTCCACCCCGG	CCGCCAGCCCCGGCTCCCCCCCCCCCCCCCCCGCGCCGCGCCCAAGCGCAGGGGC 606	
\ 6 6	181 SerSerGly           607 TCCTCGGGC	'SerValValValAsp 	LeuLeuTyrTrpArgA 	erSerGlySerValValValBapLeuLeuTyrTrpArgAspIleLysLysThrGlyVal 200 	
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l &		lleAlaLeuAlaLeu	LeuSerValThrileS	24	
qa	727 ACAGCCTAC	ATTGCCTTGGCCCTG	CTCTCTGTGACCATC		_
<u>ک</u> ک		AlaileGinLysser	AspGluGlyHisProF	ValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 260	
g 2	787 GIGAICCAA	GCTATCCAGAAATCA	saigaagsccacccai valginivatvrser	rrcaggcaratriciggaricr 846 SerslatanglyHiaval 280	
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දි සි	281 AsnCysThr 	:lletysGluLeuArg	ArgLeuPheLeuValA 	AsnCysThrIleIvsGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 300 	
õ,	01	aValLeuMetTrpValPheThrTyrValGlyAl	PheThrTyrValGlyA	32	

Search completed: August 3, 2005, 23:12:11 Job time : 4346 secs

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US-09-580-923-34
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12, Appli
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10, Appli
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                                                                                     August 3, 2005, 17:11:04 ; Search time 376 Seconds (without alignments) 9748.032 Million cell updates/sec
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Sequence 17, Appl
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Sequence 36,
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. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
.: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
.: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
.: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
.: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-860-923-17
US-08-860-923-17
US-08-979-608A-36
US-09-517-849-36
US-09-517-849-36
US-09-517-849-36
US-09-517-849-30
US-08-979-608A-30
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US-08-979-608A-30
US-08-956-1718-2153
US-08-956-1718-2153
US-08-713-986A-2153
US-08-113-646A-40
US-08-113-646A-38
US-09-930-181-14
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                                                                                                                                                                                                                                   1202784 seqs, 818138359 residues
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Maximum Match 100%
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Match Length
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14612, Appl
6, Appli
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APPLICANT: Scherman, Daniel
APPLICANT: Scherman, Daniel
APPLICANT: Wils, Pierre
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURETION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: PURETION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: PURETION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: PURPERSON OF SCHOOL OF SCHOOL
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Patent No. 6287762
GENERAL INFORMATION:
APPLICANT: CROUZET, Joel
APPLICANT: SCHERMAN, Daniel
APPLICANT: WILS, Pierre
ITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION
ITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 48;
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; OTHER INFORMATION: oligonucleotide
US-09-580-923-34
US-09-827-289-17
US-09-36-290-36
US-09-306-290-36
US-09-120-85-3
US-09-120-85-3
US-09-101-751A-14
US-09-101-751A-14
US-09-590-211A-6
US-09-590-211A-8
US-09-21B-207-275
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US-08-941-445A-29
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Best Local Similarity 87.2%; Pred. No. 12;
Matches 41; Conservative 0; Mismatches
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REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 10797-002001 (formerly 3983/59818)
TELECONTRICATION: 1NFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 36:
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ZIP: 02110-2804

COMPUTER READABLE PORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/979, 608A

FILING DATE: 26-NO. 6355451-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/048,547

FILING DATE: 03-JUN-1997

APPLICATION NUMBER: US 60/031,930

FILING DATE: 27-NOV-1996
         ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: oligonucleotide US-09-580-923-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
TREATING ATHEROSCLEROSIS
                                                                                                    Score 37.4; DB 3;
Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35.2; |
Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1...48
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coding Sequence
                                                                                                                                                                                                                                                                                                   RESULT 4
US-08-979-608A-36
; Sequence 36, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.6%;
                                                                                                      Query Match
Best Local Similarity 87.2%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-979-608A-36
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APPLICANT: Wile, Pietre.
APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: IMMOBILIZED OLIGONUCLECTIDE
FILE REPREBLACE: 03804.0138-01
CURRENT FILING DATE: 2000-05-26
PRIOR PRICK TLING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: 08/860,038
PRIOR FILING DATE: 1995-11-08
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 50;
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                                                                                                                        ZIP: 119426

ZIP: 19426

MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/860,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.7%; Score 37.4; D
Best Local Similarity 87.2%; Pred. No. 12;
Matches 41; Conservative 0; Mismatches
                  ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: SAVIEARY ESQ., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 29,699
TELECOMUNICATION INFORMATION:
TELEPANE: (610) 454-3816
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Oligonucleotide"
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: FR 94/15162
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION UNBER: WO FR95/01468
FILING DATE: 08-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09580923
Patent No. 6319672
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crouzet, Joel
Scherman, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-860-038-17
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                                                             CITY: CO
STATE: P
COUNTRY:
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APPLICANT:
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DB 4; Length 48;
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1.6%; Score 35.2; D
Best Local Similarity 83.3%; Pred. No. 41;
Matches 40; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
FRIOR APPLICATION NUMBER: US 09/517,849
FRIOR FILING DATE: 2000-03-02
FRIOR APPLICATION NUMBER: US 08/979,608
FRIOR FILING DATE: 1997-11-26
FRIOR FILING DATE: 1997-11-26
FRIOR APPLICATION NUMBER: US 60/031,930
FRIOR FILING DATE: 1997-06-03
FRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PSELSEQ for Windows Version 4.0
SSOFTWARE: PSELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Granaban, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-08-068-747-9/c
                                                                                                                                                                                                                                                                                                                                                                US-09-616-289-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                   Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36, Application US/09616289
Patent No. 6632923
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.6%; Score 35.2; DB 4; Length 48; 83.3%; Pred. No. 41; tive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1814 & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Coding Sequence
LOCATION: 1...48
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INPORMATION:
                                                               Sequence 36, Application US/09517849
Patent No. 6605588
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                Simon W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 83.3
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
                     RESULT 5
US-09-517-849-36
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US-09-616-289-36
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Sequence 9, Application US/08068747

Sequence 9, Application US/08068747

Patent No. 5695933

GENERAL INFORMATION:

APPLICANT: Schalling, Martin

APPLICANT: Hudson, Thomas J.

TITLE OF INVENTION: Direct Determination of Expanded

TITLE OF INVENTION: Nucleotide Repeats in the Human Genome

TITLE OF INVENTION: Nucleotide Repeats in the Human Genome

CORRESPONDENCE ADDRESS:

ADDRESSE: 11

CORRESPONDENCE ADDRESS:

ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE Massachusett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
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Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
RADRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
                                                                                      Law, Simon W.
                                                                                                                                                                                           NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-09-616-289-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
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                                                                                                                                                                                                                                 Sequence 30, Application US/08979608A

Patent No. 6355451
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 30:
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 GAGGAGGAAGAAGAGGAGGAGGAGGAGGACGAGGACGAAGA 280
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAAGAGGAAGAAGATGATGAAGATGAAGATGAAGATGA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILLING DATE: 26-No. 6355451-1997
PRIOR APPLICATION DATA:
                                                                                                                    87.2%; Pred. No. 3.7e+02;
tive 0; Mismatches 5;
                                                                                      232 AGGACGAGGAGGAGAAGAGAGGAGGAGGAGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1...45
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 42
                          Best Local Similarity 87.23
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                RESULT 8
US-08-979-608A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-979-608A-30
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APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Law, Simon W.

APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: ATHEROSCIEROSIS

TITLE OF INVENTION: ATHEROSCIEROSIS

TITLE OF INVENTION: NUMBER: US/09/616,289

CURRENT FILING DATE: 2000-07-14

PRIOR PEPLICATION NUMBER: US 09/517,849

PRIOR PELLING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 08/979,608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.2%; Score 28; DB 4; Length 45; Best Local Similarity 77.3%; Pred. No. 2.2e+03; Matches 34; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 GAGGAGGAAGAAGAGGAGGAGGAAGAGGACGACGAAGA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAAGAGGAAGATGATGATGAAGATGAAGATGAAGAAGATGA 44
STATE: MA
COUNTRY: USA
ZIP: O2110-2804
ZIP: O2110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compactible
COMPUTER: IBM Compactible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
FRIOR APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1...45
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application US/09616289 Patent No. 6632923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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RESULT 9 US-09-517-849-30 'Sequence 30, Application US/09517849 'Patent No. 6605588

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JS-08-956-171E-2153
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APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
TAPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 GAGGAGGAAGAAGAGGAGGAAGAAGAGGAGGACGAGGACGAAGA 280
                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.2%; Score 28; DB 4; Length 45; Best Local Similarity 77.3%; Pred. No. 2.2e+03; Matches 34; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "product = "old linker/
protein info: old linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:

CLASSIFICATION: 424

RIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967

FILING DATE: 06-FBE-1992
ATTORNEY AGENT INPORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829

REGISTRATION NUMBER: 27,829

REGISTRATION NUMBER: 27,829

REGISTRATION NUMBER: 27,829

REGISTRATION STATEMENT ON:
TELEPHONE: (617) 248-7000

TELEPHONE: (617) 248-7000

TELEPHONE: (617) 248-7100

TELEPHONE: (617) 248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/08356786 Patent No. 5877305 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COCATION: 1..45
CTHER INFORMATION:
CTHER INFORMATION:
US-08-356-786-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                    US-09-616-289-30
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US-08-356-786-13
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                                                                                                                                                                                                  SEQ ID NO 30
LENGTH: 45
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Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5.56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                          US-09-513-999C-30835/C

US-09-513-999C-30835/C

Sequence 30835, Application US/09513999C

Patent No. 678361

APPLICANT: Duclert, A.

APPLICANT: Duclert, A.

TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PAPLICANT: Glordano, J.Y.

TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PAPLICANT: Glordano, J.Y.

TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PAPLICANT: Glordano, J.Y.

PARLING DATE: 209-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER: PATENT P
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                                                                                               Gaps
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Query Match 1.2%; Score 27.6; DB 2; Length 45; Best Local Similarity 78.6%; Pred. No. 2.7e+03; Matches 33; Conservative 0; Mismatches 9; Indels
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Pred. No. 7.9e+03;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 ACGCGCCCCGGCGCGCGCGCAGCTGCAGCATCATCTCCAC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 AAGCGGCGGCGCGCGCGCAACGGCAGCGCCGCCTCCTCAAC 3
                                                                                                                                                                                     233 GGACGAGGAGGAAGAAGAGGAGGAAGAGGAGGACGAGGA 274
                                                                                                                                                                                                                                                                      1 GGAGGAGGAGCATCTGGAGGAGGACCTGGAGGAGGAGGA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2153, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.2%;
Best Local Similarity 73.3%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-30835
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US-08-781-986A-2153
US-08-781-986A-2153
Sequence 2153. Application US/08781986A
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                617 CCCGCCAGCCCCGGCTCCCGCGCGCCCCCTCCACCCCGGCCGCGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.1%; Score 25.6; DB 4;
Best Local Similarity 69.4%; Pred. No. 8.8e+03;
Matches 34; Conservative 0; Mismatches 15;
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELEPHONE: (240) 314-1224
TELEPHONE: (240) 314-1224
TELEPRAX: (301) 309-8339
INFORMATION FOR SEQ ID NO: 2153:
SEQUENCE CHARACTERISTICS:
LENDER RESERVED TO NO: 2153:
SEQUENCE CHARACTERISTICS:
LENDER RESERVED TO NO: 2153:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 2153: US-08-956-171E-2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2153:
                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 69.4
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Gaps

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                                     Sequence 4, Application US/08068747

Patent No. 5695933
GENERAL INFORMATION:
APPLICANT: Schalling, Martin
APPLICANT: Housman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.1%; Score 25.2; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 8.1e+03;
Matches 27; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Hamilton Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusett
COUNTRY: USA
ZIP: 02173
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Grannham, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 AGGAGGAAGAGAGGAGGAGGAAGAGAGAGG 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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score:

Perfect

Sequence:

OM protein

Run on:

Scoring table:

Total number Minimum DB 8 Maximum DB 8

Searched:

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Aac64406 Human Nog
Adf62860 Human apo
Adk620133 DNA encod
Aak94408 Human ful
Ad131137 Ful1 leng
Aad68386 Human Gec
Aac56886 Human MAG
AAF60134 Human NOG
AAF60134 Human neu
Ado07886 Human NOG
AAG45550 Human nog
AAG13772 Human DNA
AAG13574 Renal cel
AAG31574 Human Eel
AAG45571 Rat NogoA
AAG16433 CONETUCT
AAG464631 Rat neuri
AAG45571 Rat NogoA
AAG01173 Rat neuri
AAG45571 Rat neuri
AAG45571 Rat neuri
AAG45571 Rat neuri
AAG45571 Rat neuri
AAG68600 Rat neuri
AAG688 Mouse pol
AAG1725 Human sec
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Add01174 Bovine ne
Aa198079 Human neu
Aa1980323 Human NGG
Aa72983 Human NGP
Aax23695 Human NSP
Aax04379 Human NSP
Adx14166 Human aut
Aax14166 Human aut
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Aav30920 Human sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human MAGI polypeptide variant encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "MAGI polypeptide"
                                                                                                                                                                 ABN86601
ADO07886
ADR13965
ADP45550
AAS09453
ACC81048
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ABV94680
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ADR83534
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ABS70449
ABX34563
ADQ16433
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AAD01173
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ADO07888
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ADQ16423
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ADK14166
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      Command line parameters:
-MODEL=frame+ par.model -DEV=xlp
-MODEL=frame+ par.model -DEV=xlp
-MODEL=frame+ par.model -DEV=xlp
-De_Cgnz_1/UGFPG spool_p/US09544776/runat_03082005_181344_28194/app_query_fasta_1.519
-De_Cgnz_1/UGFPG spool_p/US09544776/runat_blosm.rng -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bite -STRAT=1 -END=-1 -MATRIX=blosm.mo2 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE-pct -THR MAR=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLENE0 -MAXLENE=200000000
-USRE=US09544776 @CGN 1 1 708 @runat_03082005_181344_28194 -NCFU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NGG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPDEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DBLEXT=7
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Aaf90325 Human NOG
Aba05903 Human RTN
Aaz36230 CDNA enco
Abv94681 Human pan
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(c) 1993 - 2005 Compugen Ltd.
                                                                                    nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                The invention relates to human MAGI protein, which is similar to neuroendocrine-specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleoided is also useful for chromosome localization and for tissue expression studies. The present sequence represents a DNA encoding the human MAGI protein variant
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                                                                                                                               Novel polypeptides related to neuroendocrine-specific proteins and polynucleotides useful for diagnosis of various diseases and for treatment of cancer and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                    Sequence 1122 BP; 224 A; 339 C; 316 G; 243 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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99GB-00016898
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Percent Similarity:
Best Local Similarity:
                                                                                                     P-PSDB; AAY56969.
                                                          Michalovich D,
 19-JUL-1999;
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New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.
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Disclosure; Page 27; 25pp; English

The present sequence is that of cDNA encoding human NOGO-B (see AAB82350). NOGO-B is a previously known splice variant of the human NOGO gene on chromosome 2p21. The invention relates to a novel NOGO gene splice variant, NOGO-C (see AAF90323). It provides NOGO-C polypeptides ond polymucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polymucleotides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders. Also produced are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and diagnostic assays for detecting diseases associated with inappropriate NOGO-C activity or levels

Sequence 1122 BP; 224 A; 339 C; 316 G; 243 T; 0 U; 0 Other;

1122	370	0	m	0	0
Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.01e-75					4
Alignment Scores: Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

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US-09-544-	-776-2 (1-373) x AAF90325 (1-1122)
ò	1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln 20
qq	1 ATGGAAGACCTGGACCTCTCTCTTGTTCTTCGGACAGCCCACCCCGGCGCGCG 60
È	21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGluGluGlu 40
QQ	61 CCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCCGAGGACGAGGAAGAAGAAGAAGAAGAGAGAGAGAGAGAGAGAGAGA
È	41 GluGluGluAspGluAspGluAspLeuGluGluIeuGluValLeuGluArgLysProAla 60
Ωp	121 GAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGGAGGAAGCCCGCC 180
È	61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAap 80
QQ	181 GCCGGGCCCCGGGCCCCAGTGCCCACCCCCCTGCCGCGCGCCCCCTGATGGAC 240
È	81 PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal 100
Dþ	241 TTCGGAATGACTTCGTGCCGCCCCCGGGGACCCCTGCCGGCCG
ò	101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120
qq	301 GCCCGGGAGCGGCAGCCGTTTTGGGACCCGGAGCCCGGTGTCGTCGTCGTGCCCGGCGCA 360
Š	121 SerPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspAspGluProPro 140
QQ	361 TCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGACGACCTCCG 420
Š	141 AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160
Dp QD	421 GCCCGGCCTCCCCCCCCCCCCGGCCAGAGCCCCCCAGGCAGCCCCGTGTGTGT
š	161 ProproAlaProAlaProAlaAlaProProSerThrProAlaAlaProLysArgArgGly 180
qq	481 CCGCCAGCCCCGGCTCCCGCCCCCCCCCCCCCGGCCCCCAAGCGCAAGGGG 540
ò	181 SerSerGlySerValValValAspLeuLeuTyrTrpArgAsplleLysLysThrGlyVal 200
Op	541 TCCTCGGGCTCAGTGGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTG 600

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ò	201 ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal 220
QQ	601 GTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTA 660
ò	221 ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArg1leTyrLysG1y 240
ф	661 ACAGCTACATTGCCTTGGCCTGCTCTGTGACCATCAGGTTTAGGATATACAAGGGT 720
Š	ValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 26
q <sub>Q</sub>	721 GTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCT 780
ò	261 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 280
qq	781 GAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTG 840
ठे ह	281 AsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 300
g	** PACIGCACGAIAAAGGAACICAGCCCCCICIIAGIIGAIIGA
රි සි	301 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 320
8	21 LeuLeulleLeuAlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGln 34
qu	961 CTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT
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g	GCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAA TO
<i>&amp;</i> ₽	361 IleGlnalaLyg1leProGlyLeuLysArgLysAlaGlu 373 
RESU ABAU ID	Л.Т. 3 15903 ABA05903 standard; cDNA; 1216 BP.
¥ X	ABA05903;
X E i	04-MAR-2002 (first entry)
X E	luman RTN4B encoding
ŽŽ;	luman; RTN4B; gene; ss.
<b>3</b> 83	HOMO!
********	Key Location/Qualifiers CDS 51126 /*tag= a /product= "RTN4B"
X & ;	N1311439-A
X & ;	5-SEP-2
X & S	12-MAR-2000
\$ E \$	)2-MAR-2000; 2000CN-0011179
<b>(8)</b>	(UYFU-) UNIV FUDAN.
<b>\$</b> II \$	Yu L, Fu Q, Zhao Y;
\$88\$	PP 1 2002-049934/07.
<b>\$</b>	Human RTN 4B protein and coding sequence, its preparation and use.

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| LeuLeulleLeuAlaLeulleSerLeuPheSerValProValIleTyrGluArgHisGln 340
                                                                                                     LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr
GAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTG
                                             AsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu
                                                            AAGTTTGCAGTGTTGATGTGGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bone marrow secreted protein; bone marrow stromal cell; cytokine; cell proliferation; cell differentiation; hemaclopicatis; namemia; myeloid cell deficiency; lymphoid cell deficiency; myeloid cell; colony stimulating factor; granulocyte; erythroid progenitor cell; colony stimulating factor; granulocyte; monocyte; myelo-emptyression; megakaryocyte; platelet; platelet disorder; thrombocytopenia; hematopositic stem cell; stem cell disorder; aplastic anaemia; bone differentiation; paroxyman locturnal hemoglobinuria; bone graveth; cartilage; tendon; ligament; nerve; wound healing; tissue repair; burn; incision; ulcer; bone fracture; cartilage damage; artificial joint; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human polynucleotide and secreted proteins can induce production of other cytokines in certain cell populations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding a bone marrow secreted protein designated BMS112.
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98US-0101603P.
98US-0102540P.
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P-PSDB; AAY53624.
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24-SEP-1998;
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                            The invention relates to human RTN4B protein and coding sequence, useful for providing a cDNA sequence of human RTN4B. The protein is an isomer of RTN4 with RTN family members. The present invention also refers to polypeptide encoded by a nucleotide sequence and manufacturing method and application of the polypeptide and polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244
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                                                                                                                                                                                                                                                                                                                                                                                                                                      125 GAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGGAGGAAGCCCGCC 184
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370
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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   Page 20 (Disclosure); 27pp; Chinese
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Best Local Similarity:
                                                                                                                    Sequence 1216
                                                                                                                                               Alignment Scores:
Pred. No.:
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ABV94681 standard; cDNA; 2235
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2001US-027568P.
2001US-0287112P.
2001US-0291611P.
2001US-0305484P.
2001US-0313999P.
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09-FEB-2001; 2
21-MAR-2001; 3
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16-MAY-2001;
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27-NOV-2001;
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PR 31-

PR 91-

PR 9
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                                AZ36228-49 encode bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines, celficiencies. In addition, they may be used to support the growth and proliferation of support the growth and proliferation of myeloid cells such as anaemias. They can have colony stimulating factor (CSF) activity and can consemias. They can have colony stimulating factor (CSF) activity and can anemias. They can have colony stimulating factor (CSF) activity and can consemia, thereby allowing prevention of myeloid cells such as granulocytes, monocytes or macrophages, to prevent or treatment of platelet can platelets, thereby allowing prevention of reatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of hematopoeitic stem cells, either in place of or in conjunction with platelet transfusions, to treatment of platelet, or to recopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers, to induce cartilage and/or bone growth in circumstance where bone is not normally formed and thus have an application in healing bone fractures and cartilage and thus have an application in healing bone fractures and cartilage and thus have an application in healing bone fractures and cartilage damage or defects, prophylactic use in fracture.
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Claim 11; Page 72-74; 120pp; English.
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612 CCGCCAGCCCCGGCTCCCGCCGCCCCCTCCACCCCCGGCCGCCCCAAGCGCCAGGGGC
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The invention relates to an isolated polynucleotide (1) comprising: (a) any of a group of over 4000 nucleotide sequences (ABY94628-ABY99145); (b) complements of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences having at least 75% or 90% identity conditions; (e) sequences having at least 75% or 90% identity conditions; (e) sequences having at least 75% or 90% identity conditions; (e) sequences having at least 75% or 90% identity conditions; (e) sequences having at least 75% or 90% identity conditions; (a) and oligonucleotide can be used to detect cancer conditions; (b) and oligonucleotide can be used and thindles, fusion proteins, T cell populations and antigen presenting antimumer response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and properties and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                        New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic
                                                 Υ;
                                                 Jiang
                                                 Lodes MJ, Persing DH, Hepler WT,
                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 54; 300pp + Sequence Listing; English.
                                              Kalos MD,
(CORI-) CORIXA CORP.
                                                                                             WPI; 2002-627435/67.
P-PSDB; ABP68601.
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Sequence 2235 BP; 562 A; 560 C; 537 G; 576 T; 0 U; 0 Other;

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Length:
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Mismatches:
Indels:
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21-JUN-1999;
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The present sequence encodes a human stress-phosphorylated endoplasmic reticulum protein, designated Nogo B. Nogo B has cytostatic activity and is a modulator of the storage and exchange of calcium, cell growth and cellular stress response. It can: regulate oxidative stress; inhibit neutrite outgrowth, neuron growth and axon regeneration. Nogo B polypeptides and polynucleotides are useful for modulating stress levels and cellular stress-response, cell growth and viability, diagnosis and treatment of cancer, malignant growth and other Nogo B related diseases. Nogo B polypeptides are also useful to screen combinatorial libraries to identify agonist or antagonist. Antibodies against Nogo B polypeptides are useful for affinity chromatography and distinguishing Nogo B polypeptides
                                                                                                                                               Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.
                                                                                                                                                                                                                                      Claim 2; Page 63-64; 68pp; English.
                                           Williams LT;
                                         Halenbeck R,
                                                                                    WPI; 2000-665007/64
(CHIR ) CHIRON CORP
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ÖS	SQ Sequence 2240 BP; 570 A; 558 C; 536 G; 576 T; 0 U; 0 Other;	2240	BP;	570	Ą	558	່ວ	536	ΰ	576	Ë	0	;	0	)ther;	
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AlaProGluhrgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120 ProProAlaProAlaProAlaAlaProProSerThrProAlaAlaProLysArgArgGly 180 GCCGGGCTGTCCGCCGCCCCAGTGCCCACCCCCCTGCCGCCGCCGCCCCCCTGATGGAC SerPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspAspGluProPro CGGCCAGGCCCCGGGCTCCCGCCCCCCTCCACCCCGGCCGCCCCAAGCGCGCCAGGGGCC MetGluAspLeuAspGlnSerProLeuValSerSerAspSerProProArgProGln PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal GCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCCGCGCCCA GluGluGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla GAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGGAGGAGGAGGAGGCCCGCC AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr GCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTGTGGACC US-09-544-776-2 (1-373) x AAC64406 (1-2240) 138 21 198 258 61 318 378 101 141 558 41 81 438 121 498 191 a g g g ठ à 요 ò 윱 ઠે g ð 셤 ર્જ ò 8 8

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                                                                                                                                                                                                                                                                            918 GAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTG
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                    678 TCCTCGGGCTCAGTGGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTG
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This invention describes novel mucleic acid molecules that are associated with apoptosis and encode a polypeptide and are derived from a normalised apoptosis and encode a polypeptide and are derived from a normalised apoptosis measured by cell death detection assay or the CPRG assay (measuring loss of membrane integrity). The products of the invention have cytostatic, neuroprotective, immunosuppressive, antirheumatic, have cytostatic, anticonvulsant, antiparilammetory, hepatotropic, virucide, nootropic, anticonvulsant, antiparkinsonian, vasotropic, creebroprotective and antialcoholic activity and can be used for gene therapy. The polynucleotides also related vectors, hosts (or their extracts), encoded polypeptide (or their receptors) and/or agents that inhibit their activity (including antisense sequences) are used for treatment or prevention of tumours, autoimmune or degenerative diseases and viral infections, rheumatoid arthritis, diabetes, lupus, or infection with hepatitis or influenza viruses, Alzheimer's, Huntington's or Parkinson's diseases, reperfusion injury, stroke and alcoholic liver disease. Detection of the polynucleotides and derived polypeptides can appoproals—second archine described in the disclosure of the choose an experience approaches and derived polypeptides and expense.
                                                                                            New nucleic acids involved in apoptosis, useful for diagnosis and treatment of e.g. tumors and degenerative disease, also related proteins, antibodies and modulators.
Kesper
  Schaefer R,
                                                                                                                                                                                                   Claim 1b; SEQ ID NO 303; 517pp; German
Kazinski M,
                                            WPI; 2003-542134/51
Koenig-Hoffman K,
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Sequence 1599 BP; 354 A; 452 C; 422 G; 371 T; 0 U; 0 Other;

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                                                                                                        TCCTCGGGCTCAGTGGTTGTTGACCTCCTGTACTGGGAGACATTAAGAAGACTGGAGTG
GTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTA
                                       ProProAlaProAlaProAlaAlaProProSerThrProAlaAlaProLysArgArgGly
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67. .1188
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AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro
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                                                                                                                                                                                                                                                                                                        Identifying modulators of Nogo or BACE activity for treating acute neuronal injuries, neoplastic or dysproliferative disorders, comprises providing and monitoring interaction between Nogo and BACE polypeptides.
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(SMIK ) SMITHKLINE BEECHAM PLC
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                                                                                                                                                                                                                                                                      830 Primers useful for synthesizing full length cDNA clones and in genetic manipulation.
                                                                                                                                                                            Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Ko
                                                                                                                                                                                                                                                                                                                     8; SEQ ID NO 3170; 1380pp + Sequence Listing; English.
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Matches:
Conservative:
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                                                                            08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
                                              07-JUL-2000; 2000EP-00114089
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Percent Similarity:
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P-PSDB; AAM93484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein-encoding gene 42 cDNA clone HAGFT48, SEQ ID NO:52
                                                                     rLeuleulleLeuAlaLeulleSerLeuPheSerValProVall1eTyrGluArgHisGl
                                           CTCCTCGGGCTCAGTGGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                  GAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCT
                    ySerSerGlySerValValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVa
                                                                                                                                                             1ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGl
                                                                                                                                                                                                                                    240 yVallleGlnAlaIleGlnLybSerAspGluGlyHisProPheArgAlaTyrLeuGluSe
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/product= "Human secreted protein precursor"
/note= "CDS does not include start codon"
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                                                                                                                                                                                                                                                                               This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential theraspeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
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                                                                                       Kawai Y;
T, Koga 1
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                                                                                       Ishii S,
S, Otsuki
                                                                                                                                                                                         New oligonuclectide primers (830 cDNAs) useful for length human cDNAs.
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Matches:
Conservative:
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K, Kojima
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02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
                                                                                       Ota T, Nishikawa T, Isogai
Wakamatsu A, Sugiyama T, Na
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P-PSDB; ADL31138.
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AARD08345-AAD08394 represent CDNAB corresponding to 50 human secreted protein genes and AAE03898-AAE03947 represent the proteins they encode. AAE03948-AAE03996 represent human secreted protein fragments or variants. CC AAE03948-AAE03996 represent human secreted protein fragments or variants. The genes and their secreted proteins equal for preventing treating or ameliorating medical conditions, e.g., by protein or gene therapy. CC Pathological conditions can be diagnosed by determining the amount of the new genes. Specific uses are described for each of the 50 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, tumours, foetal and developmental abnormalities, haematopoietic disorders diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, contivive disorders (e.g., Alzheimer's disease, Parkinson's disease), contivive disorders (e.g., Alzheimer's disease, Parkinson's disease), contivive disorders, schizophrania, asthma, skin disorders (e.g., pregnancy-related disorders, andocrine disorders, and indepense, and continue disorders, and indepense and solve used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, corresponse tissues, to identify their cognate ligands or binding corters, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassay erg., and in the alsorate and in diagnostic and indiagnostic immunoassay erg., and in the alsorate and in diagnostic and indiagnostic immunoassay erg., and in the alsorate and in diagnostic and indiagnostic and indiagnostic and indiagnostic and indiagnostic and indiagnostic and indiagn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding 50 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases, e.g. Parkinson's disease, botulism, cancers and Scimitar syndrome.
                       /*tag= c
/product= "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                               Komatsoulis GA;
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P-PSDB; AAE03939.
                                                                                                  WO200077022-A1
                                                                                                                                                                                                                                             11-JUN-1999;
mat_peptide
                                                                                                                                             21-DEC-2000.
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Sequence 1683 BP; 369 A; 489 C; 464 G; 358 T; 0 U; 3 Other;

Pred. No.:	3.45e-68	Length:	1683
Score:	1723.50	Matches:	346
Similarity: cal Similarity:	92.768	Mismatches:	O 44 (
Query Match:	90.24 <b>%</b>	Indels:	7.
DB:	4	Gaps:	1.

US-09-544-776-2 (1-373) x AAD08386 (1-1683)

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1243 Arccaagcaaaarrccriggarrgaagcgcaaagcrgaa 1281 RESULT 12 ADB85284 ID ADB g

BP

ADB85284 standard; DNA; 2782

1132 1182 GTGATCCAAGCTATCCAGAAATCAGATGAAAGGCCACCCATTCAGGGCATATCTGGAATCT 1012 1137 1183 GCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAA 1242 300 280 340 360 412 472 100 532 120 592 140 652 160 712 180 772 200 832 220 892 240 952 260 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 320 9 80 AsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro SerPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspAspGluProPro receeererereceecaerereecerecereceaeereeeeree GCCCGGCCTCCCCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTGTGGACC SerSerGlySerValValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal 321 LeuLeulleLeuAlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGln 341 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp GCCGGGCTGTCCGCGCCCCCAGTGCCCACCGCCCCTGCCGCCCGGCGCGCCCCTGATGGAC TCCTCGGGCTCAGTGGTTGTTGACCTCCTGTACTGGAGAGACATTAAAGAAGACTGGAGTG GluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr ProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArgArgGly coaccadececederecedececececececececedececedececeaececadececadecece GIGITIGGIGCCAGCCTATTCCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTA ThralaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGly ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal ValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 361 IleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 1133 AAGCT------1013 353 61 413 81 473 533 593 653 713 773 201 221 893 953 281 301 1138 41 101 121 141 161 181 833 241 261 ò g ò ď ò 셤 ò 셤 ð 원 8 ద ર્જ 유 8 셤 δ ద ઠે g ઠે g 8 g ∂ 셤 ò 유 ે 요 8 원 8

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AAZ56886 standard; DNA; 3579
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                                                                                                                                                                                                                                                                                                                                                                    Use of gene sequence that is down-regulated in response to streptozocin-induced diabetes, vector, host cell, animal, polypeptide and antibody, in screening of compounds for treating or diagnosing pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulated in the spinal confine the spinal confine to streptozocin-induced diabetes, or comprising, hybridising or having at least 80% sequence identity to a sequence whose expression products are kinases, phosphatases, ion channel proteins, receptors, transporters, G-protein coupled receptor proteins, DNA-binding proteins, proteases or enzymes, given in the specification. A gene of the invention has analgesic activity, and may have a use in gene therapy. The gene sequences, vector, host cell, animal, polypeptide and antibody are useful for screening of compounds for diagnosing or treating pain. The kits are useful for simultaneous, separate or sequential detecting and/or quantifying down-regulation of a gene sequence in the spinal cord of a mammal in response to streptozocin-induced diabetes. The compound or pharmaceutical composition is useful as a medicament for treating or diagnosing pain. The present sequence represents a gene of the invention.
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                                                                                   rat; streptozocin; kinase; phosphatase; ion channel protein; receptor; transporter; G-protein coupled receptor; GPCR; DNA-binding proteins; protease; enzyme; analgesic; gene therapy; pain; diabetes; ds; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to a novel isolated gene sequence that is down-
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Conservative:
Mismatches:
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1021 CATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGATGAAGTTGTG 1080
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                                                                                                                                                                                                                                      MAGI protein; neuroendocrine-specific protein; neuropathy; human; spinal injury; neuronal degeneration; neuromuscular disorder; cancer; psychiatric disorder; developmental disorder; inflammatory disorder; stroke; cytostatic; cerebroprotective; neuroprotective; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptides related to neuroendocrine-specific proteins and polynucleotides useful for diagnosis of various diseases and for treatment of cancer and neurological disorders.
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è	185 185	2341	GAATATGAAAATAAAGGAAAAACTCAGTGCTTTTGCCACCTGAGGAGGAAAGGCCATATTG 2400
qq	1261 GATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAAAATAGTGAGAGT 1320		
à	185 185	T83	
ΩÞ	1321 AGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGATCGTCCAGGAGCA 1380	2401	GARICITITARGCICAGITIAGAIAACACAAAAGAIACCCIGITACCIGAIGAAGITICA 2460
È	185 185	185	
qq	1381 TATATCACATGTGCTCCCTTTAACCCAGCAACTGAGAGCATTGCAACAACATTTT 1440	2461	ACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTCAGTACTGCAGTTTAT 2520
ò	185 185	185	
q	1441 CCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACGATGAAAAAAAA	2521	TCAAATGATGACTTATTTTTTTAAGGAAGCACAGATAAGAAAACTGAAACGTTTTCA 2580
È	185 185	185	
QQ	1501 AAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAACCTTTTCTTGTA 1560	2581	GATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATCAGTTCTAAAACTGAT 2640
à	185 185	185	
d d	1561 GCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACAAAGGTGACTGAG 1620	2641	TCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCCACAAAAGTGAAATT 2700
ò	185 185	185	
d d	1621 GAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAGGAAGCATGTGAA 1680	2701	GCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACAGAATTGCCCCATGACCTTTCT 2760
ò	185 185	185	
qq	1681 AGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAACAAAATGGACTTGGTT 1740	2761	TTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGATGACTTTTCTAAA 2820
ò	185 185	185	
g	1741 CAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTTTGCCCATCATTT 1800	2821	AATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCTGCTTTGGCCACT 2880
ò	185 185	185	185
q	1801 GAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATGGAAGCACCAFTG 1860	2881	CAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAGAAGCTGAGAAAAA 2940
ò	185 185	185	
qq	1861 AATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCATCACCATTAGAA 1920	2941	
ò	185 185	186	ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValVal 201
q	1921 GCTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAACCCCCCCC	3001	
ò	185 185	Oy 202 PheGlyAlaSer	Phed.yAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerTleValSerValThr 221
q	1981 GAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAAGAAATTAAAGGCCT 2040	Tans	
ò	185 185		Atarianterialeurianeurianeuria (a. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.
qa	2041 GAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATTGCATGTGAT 2100	242	
ò	185 185	3181	ATCCARGUE TO CORRESPONDE DE LA COMPTENDA SE LA COMPTENDA DE COMPTENDA SE LA COMPTENDA DE COMPTENDA SE LA COMPTENDA DE COMPTENDA DECOMPTENDA DE COMPTENDA DECOMPTENDA DE COMPTENDA DECOMPTENDA DE COMPTENDA DE COMPTEN
ф	2101 TTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTCTCTGATTATTCAGAA 2160	290	
ò	185 185	3241	ATTITUTE TO CONTROLLED TO CONT
qq	2161 ATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTTGAAGATTCCTCACCT 2220	280	
È	185 185	3301	TICLE CONTROLL OF THE CONTROL
q	2221 GATICTGAACCAGTIGACTTATTTAGTGATGATTCAATACCTGAGGTTCCACAAAAACAA 2280	202	
ò	185 185	302	FIGHTA VALLEGUECTE D'OLTRE CONTROLLE D'ANNO CONTROLLE DE L'ANNO CO
q	2281 GATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTTGAGTCAATGATA 2340	322	

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3481 CAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAT 3540
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                                                                                                        GlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIle 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease; neuromuscular disorder; psychiatric disorder; developmental disorder; neuropyrotective; nootropic; neuroleptic; antiparkinsonian; cerebroprotective; neuroleptic; diagnosis; therapy; ss.
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                                                                                                                                                                                                                                                                                                                     3541 CAAGCAAAATCCCTGGATTGAAGCGCAAAGCTGAA 3576
                                                                                                                                                                                                                                                    GlnAlaLysIleProGlyLeuLysArgLysAlaGlu 373
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24-JAN-2000; 2000GB-00001550.
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q	1501 AAGGCCCAAATAGTAACAGAAGAATACTAGCACCAAAACATCAAACCTTTTCTTGTA 1560	2581	GATICAICICCAATIGAAATTATAGAIGAGTICCCTACATIGAICAGTICTAAAACIGAT 2640
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qq	1561 GCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACAAAGGTGACTGAG 1620	2641	TCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCCACAAAAGTGAAATT 2700
à	185 185	Qy 185	185
셤	1621 GAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAGGAAGCATGTGAA 1680	2701	GCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACAGAATTGCCCCATGACCTTTCT 2760
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qq	1681 AGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAATGGACTTGGTT 1740	2761	TIGAAGAACATACAACCCAAAGTIGAAGAAAATCAGTITCTCAGAIGACTITTCTAAA 2820
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qq	1921 GCTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAACCCCCCCACCATATGAA 1980	1005	
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qq	2041 GAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATTGCATGTGAT 2100	242	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stroke; peripheral nerve damage; neoplastic disorder; glioblastoma; neuroblastoma; hyperproliferative disorder; dysproliferative disorder; cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer; tissue hypertrophy; central nervous system; axon regeneration; NogoA; Nogo-associated disease; metastasis; gene; ds.
                                                                                              GTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAC
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/*tag= a /product= "Human NogoA protein"
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(SMIK ) SMITHKLINE BEECHAM PLC.
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The present invention relates to a new method of identifying modulators of Nogo function or BACE activity. The method involves providing Nogo and BACE proprieties capable of binding with each other, monitoring the interaction between these polypeptides, and determining if the test agent is a modulator of Nogo or BACE activity. The method is useful in treating caute neuronal injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas). peripheral nerve damage, and in neoplastic (e.g. glioblastomas, contribusis, psoriasis, keloid formation, fibrocystic conditions, tissue hypertrophy) of the central nervous system. The BACE polypeptides is useful in screening methods to identify agents that may act as modulators of BACE activity and in particular agents that may be useful in treating now associated diseases. The modulators of Nogo or BACE polypeptides, and the polymucleotide encoding the BACE polypeptide are useful in manufacturing a medicament for the treatment or prevention of disorders responsive to the modulation of Nogo activity, in alleviating the symptoms or improving the condition of a patient suffering from this disorder, in axon regeneration, or in preventing metastasis or spreading of assays, a probe, in recombinant protein synthesis, and in gene therapy techniques. The present nucleic acid sequence encodes the human NogoA
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Search completed: August 3, 2005, 23:25:47 Job time: 606 secs

protein

Run on:

Sequence:

Perfect

Minimum DB Maximum DB

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AK034902

Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430059L06 product:RETICULON 4 (NEWRITE OUTGROWTH INHIBITOR) (NOGO PROTEIN) (FLOCEN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog [Rattus
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(c) 1993 - 2005 Compugen Ltd.
                                                                       nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                    The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3533)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKRN), Laboratory for Genome Exploration Research (STERN) Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yolivake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B., Watchiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J. Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKBN integrated sequence analyais (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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PROTEIN) (FOOCEN) (GLOTY VESICLE 20 KDA PROTEIN)
[Rattus norvedicus] (SWISSPROT|(99XI1, evidence:
95.8%ID, 100%length, match=1068)"
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URL.http://genome.gsc.riken.jp/
URL.http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Mismatches:
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/mol type="mRNA"
/strain="C57BL/6J"
/db_xref="FaNTOM DB:9430059L06"
/db_xref="taxon:10090"
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequeségenoscope.cns.fr, Web : www.genoscope.cns.fr plat strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library
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AL549191 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COT 25-NORMALIZED Homo sapiens CDNA COTONE CSODIO51YB11 5-PRIME, mRNA sequence.
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1 (bases 1 to 911)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization
On Peb 15, 2001, On Peb 15, 2001, this sequence version replaced gi:31271011.
                                                                                                                                                                                                                                                                      ThralaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGly
                          AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp
                                                                                                        PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal
                                                                                                                                               101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On May 15, 2003 this sequence version replaced gi:30787776.

Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Smail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and BcoRV sites of the pCWVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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/clone lib="Homo sapiens PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoNV sites of the pCMVSPORT 6 vector.
                                                                                                                                                                                                       BX439214 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE008YG04
5-PRIME, mNA sequence.
BX438214
                          CAGGCGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGCGTTAAGGATGCCATGCC 1261
GlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAla 359
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 1097)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence belongs to sequence cluster 1423.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE008BD02QPl&c=1423.r.
Location/Qualifiers
                                                                                                          LyslleGlnAlaLyslleProGlyLeuLysArgLysAlaGlu 373
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Matches:
Conservative:
Mismatches:
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BIO79496 781 bp mRNA linear EST 20-JUN-2001 602876306F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5008248 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The J.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Consortium (LLNL)
The found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11052 row: k column: 01
High quality sequence stop: 773.
Location/Qualifiers
I. 781
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//gtrain="FVB/N-3"
//gtrain="FVB/N-3"
                                /clone_lib="NCI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCWV-SPORT6; Site 1: Sall;
/note="Organ: mammary; Vector: pCWV-SPORT6; Site 1: Sall;
Site_2: Not!; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Musmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 781)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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           220 lThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGl
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                                                                                  240 yValileGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGlu
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1138.50
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                                                                                                                                      /organism="Homo sapiens"
//mol type="mRNA"
//db xref="taxon:5606"
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/clone lib="Homo sapiens Placenta COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
/primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECRN V sites of the pCMVSPORT 6 vector. Library was normalized."
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was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1423.r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 IleTyrLysGlyVallleGlnAlalleGlnLysSerAspGluGlyHisProPheArgAla
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Conservative:
Mismatches:
     -minmatch
by cross_match using options -minmatc
Plate: 41 row: O column: 13
Seq primer: CCTATTAGGTGACACTATAGAAC
High quality sequence stop: 677.
Location/Qualifiers
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P.
Matukumalli, L.K.
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Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
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                            GGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGGAGGAGGAGCCCGC 324
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 924)
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                                                                                                                                                                                                                                                                                                                                         505 ATCCCCGCTGTCTGCCGCACTCTCGCCCTCCAAGCTCCCTGAGGACGACGACGAGCCTCC
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                                                                                                                                                          pPheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProProVa
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  uGluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAl
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National Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CONA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AWAMAATAAWTTTKSTCYTTGGKCATDTTKAAWTHSACVAWAAAARAAWCAAGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Genoscope Control of Sequencage Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr lst strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRY sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol.type="mixtor" or process
/mol.type="mixtor" or process
/colne="CSODG002YP16"
/coll line="RAMOS CELL LINE"
/coll line="RAMOS CELL LINE"
/colne_line="RAMOS CELL LINE"
/colne_line="RAMOS CELL LINE"
/colne_line="New or priens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into Library was not normalized."
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1. (bases 1 to 1002)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)

On May 22, 2003 this sequence version replaced gi:31035379.
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BX462171 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA clone CSODG002YP16 5-PRIME, mRNA sequence.
                                                             609 GAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGAT
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                                         GluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              division of Invitrogen.
This sequence belongs to sequence cluster 1423.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODG002DH08QP1&c=1423.r.
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/dev stage="10 months"
/lab_host="bH108"
/lab_host="bH108"
/clone lib="NLC GAAP Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                       BI157842 108-JUL-2001
602923001F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5062944 5',
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 708)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov
Plate: LLAM1170 row: b column: 01

High quality sequence stop: 708.
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                                                                                                                                                  703 CATCAGGCACAGATAGATCATTATCTAGGACTTGCAAAATAAGAATGTTNAAGATGCTATG
    523 CATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGAT
                                                                                      583 TCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGT
                                                                                                                           319 LeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArg
                                            299 SerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGly
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Indels:
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/strain="129,C57BL/6J,FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:5062944"
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Mus musculus
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BI157842.1 GI:14617843
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                                                                                                                                                               /organism="Homo sapiens"

// Lype="mRNN"

// Da_Tref="taxon:9606"

// Clone="InMAGE:5679264"

// Lissue_type="teratocarcinoma, cell line"

// Lone lib="NIH MGC l09"

// Lone lib="NIH MGC l09"

// Clone lib="NIH MGC l09"

// Note="Organ: ovary; Vector: pOTB7; Site_1: EcoR1; Site_2:

Xhof; cDN made by olign-dT priming. Directionally cloned linc EcoR1/Xhof sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgGlySerSerGlySerValValValAspLeuLeuTyrTrpArgAspIleLysLysThr 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 AlaAlaAlaValSerProSerLysLeuProGluAspAspGlu---------- 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 ProAlaSerValSerProGlnAlaGluProValTrpThrProProAlaProAlaProAla 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 GGCCCCGGCGGCGGCGCGCGCGCGCATCATCTCCACCCCGGCCCGGCCCCAAGCGC 222
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DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Plate: LLCM3782 row: e column: 24
High quality sequence stop: 696.
Location/Qualifiers
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/dev_stage="5 months"
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Mismatches:
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E 1 (Bases 1 to 810)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI1052 row: d column: 13

High quality sequence stop: 802.
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990 bp mRNA linear EST 18-SEP-2001 603314519F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5354477 5', BI691132
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1901 row: e column: 06
High quality sequence stop: 758.
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Location/Qualifiers
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Location/Qualifiers
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                                                                                                                               119 AcAdrarıcaGCArrereaGGGTAACAGCCTACATGCCTTGGCCCTGCTCTGTGACC
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/tissue_type="infiltrating ductal carcinoma"
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/note="Organ: Eye; Vector: pSportl; RNA was extracted from primary human pericytes in culture. A directionally cloned cDNA library in the pSPORT1 vector (invitrogen) was constructed at Bioserve Biotechnology (Laurel ND) essentially following the protocols of the SuperScript Plagmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGATCAGGAGGGCCCC(C7)15-3']. CDNA was cloned in Not 1/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                     CN482802 592 bp mRNA linear EST 26-APR-2004 hw24h12.yl Human primary human ocular pericytes. Unamplified (hw) Homo sapiens CDNA clone hw24h12 5', mRNA sequence.
                       676 CATTATCTAGGACTTGCAAACAAGAGGTTAAGGATGCCATGGCCAAAATCCAAGCAAAA 735
HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 ProAlaAlaProLysArgArgGlySerSerGlySerValValValAspLeuLeuTyrTrp 192
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 592)

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Expressed sequence tag analysis of cultured primary human ocular
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/dev_stage="Adult"
/lab_host="EMDH108"
/clone_lib="Human primary human ocular pericytes.
UnamplIfied (hw)"
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Section on Molecular Structure and Function
National Eye Institute
6/31, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
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Conservative:
Mismatches:
Indels:
Gaps:
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Plate: 24 row: h column: 12
Seg primer: MI3RP1 reverse primer (ABI).
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="hw24h12"
                                                                                     IleProGlyLeuLysArgLysAla 372
                                                                                                                             736 Arcccrecarreaaccccaaacc 759
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Unpublished (2004)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. 1 (Bases it of 650)

INCL-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Institute, Ph.D.

Email: cgapDs-rémail.nih.gov
CONtact: Robert Strausberg, Ph.D.
Email: cgapDs-rémail.nih.gov
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing Ds: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be infoamage. In. NGS row: G column: 23
Finfoamage.lln.gov: G column: 23
Seq primer: MIJRPI reverse primer (ABI).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      /Lissue type="normal endometrium, late proliferative phase, cycle day 13"

That host="="DH10B (T1-resistant)"
/clone lib="NICHD HS Ut1"
/clone lib="NICHD HS Ut1"
/note="Organ: uterus; Vector: pCMV-SPORT6.1.ccdb (ResGen, Invitrogen Corporation); Site_1: Not1; Site_2: EcoRV; Cloned unidirectionally from microquantity amounts of mRNA from normal endometrial tissue (late proliferative phase, cycle day 13). Average insert size 1.9 kb. Library constructed by ResGen (Invitrogen Corporation)."
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:5937070"
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CB215381 GI:28263573
EST.
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/clone_lib="NUICGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
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Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musn.

1 (bases 1 to 815)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 712.

High quality sequence stop: 712.
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                                                                                                                                                                                                                                                                      242 GCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACGAATTCT 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 TTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATT
                                                                                   176 ProLygArgArgGlySerSerGlySerValValValAspLeuLeuTyrTrpArgAspIle
                                                                                                    196 LysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPhe
                                                                                                                                                                                                         62 AAGAAGACTGGAGTGGTGCTGCTGCTTGTTCCTGCTGCTCGCTGACAGTATTC
                                                                                                                                                                                                                                                                                                                               236 ArgileTyrlysGlyValileGlnAlaileGlnLysSerAspGluGlyHisProPheArg
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neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal lleum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"
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                                       ThrLeuLeulleLeuAlaLeulleSerLeuPheSerValProVal11eTyrGluArgHis 339
                                                                                480
                                                                                                                        GlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAla 359
                                                                                                                                           361 CTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTG 420
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                Baumann, R.C., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. Matukumalli, L.K.
Matukumalli, L.K.
Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle Unpublished (2004)
Contact: Richard G. Baumann
Bovine Funcțional Genomics Lab
                                                                                                                                                                                                         LysileGlnAlaLysileProGlyLeuLysArgLysAlaGlu 373
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192
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Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
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Technologies. Note: this is a NHH_MGC Library."
                                                                                         958 bp mRNA linear EST 05-MAR-2002
AGENCOURT 6458941 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5558493
5', mRNA Sequence.
BM801698
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                                                                                                                                                                                                                                                                                    Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 958)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
High quality sequence start: 25
High quality sequence stop: 579.
Location/Qualifiers
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Site_2: NotI; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Mismatches:
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'organism="Mus musculus"
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                 /mol_type="mRNA"
/strain="FVB/N"
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Best Local Similarity:
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Search completed: August 4, 2005, 00:29:15 Job time : 3113 secs THIS PAGE BLANK (USPTO)

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e 15051, 7 e 12869, A e 10189, A 11198, A 11198, A 2, Appli 1, Appli 1, Appli 1, Appli 15, Appl 15, Appl 15, Appl 15, Appl 15, Appl

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731, 748, 4803, 4805-4806, 4808-4809
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NAME/KEY: UNBOUTE
LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 481
OCHER INFORMATION: a, t, c, g, or other
           US-09-270-767-13561
US-09-513-9997-2227
US-09-621-976-741
US-09-949-016-117589
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US-09-949-016-117589
US-09-949-016-117589
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US-07-884-811-15
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US-08-087-783A-15
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Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REWODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION UNDER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL PROGRAM
SEQ ID NO 106
LENGTH: 4822
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 Command line parameters:
-MODEL=frame+ pln.model -DEV=xlp
-MODEL=frame+ pln.model -DEV=xlp
-MODEL=frame+ pln.model -DF/859544776/runat_03082005_181346_28231/app_query.fasta_1.519
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-LIST=45 -DOCALIGN=200 -THR SCORE-pct -THF MAR=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_WMAP -LARGRQUERY -NEG_SCORES=0 -MAXIT -DSPBELOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -LONGLOG
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -FGAPOP=6
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Sequence 2, Appli
Sequence 3253, Ap
Sequence 3109, Ap
Sequence 1127, Ap
Sequence 254, App
Sequence 255, App
Sequence 258, Ap
Sequence 2988, Ap
Sequence 2988, Ap
                                                                                             August 3, 2005, 17:13:52 ; Search time 207 Seconds (without alignments) 2948.460 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                     - nucleic search, using frame_plus_p2n model
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US-09-149-476-254
US-09-949-016-298
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US-09-799-451-111
US-09-149-476-102
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Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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Jatabase :

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Result

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Oy 281 ASHCYSThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 300	341 AlaGinileAspHisTyrLeuGlyLeualaAsnLysAsnValLysAspalaMetalaLys 341 AlaGinileAspHisTyrLeuGlyLeualaAsnLysAsnValLysAspalaMetalaLys 3733 GCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAA 361 IleGinalaLysIleProGlyLeuLysArgLysAlaGlu 373	US-08-70-67-2  19.56quence 2, Application US/08700607  19.64-70-507-2  19.64-70-507-2  19.64-70-507-2  19.64-70-2  19.64-70-2  19.64-70-2  19.64-70-2  19.64-70-2  19.64-70-2  19.64-70-2  19.64-70-2  19.64-70-7  19.64-70-7  19.64-70-7  19.64-70-7  19.64-70-7  19.64-70-7  19.64-70-7  19.64-70-7  19.64-70-7  19.64-70-7  19.64-70-7  19.64-70-7  19.64-70-7  19.64-70-7  19.64-70-7  19.64-70-7  10.64-7  10.64	Alignment Scores:  Alignment Scores:  Pred. No.:  Score:  Best Local Similarity:  Query Match:  2 Gaps:  Alignment Scores:  Best Local Similarity:  Query Match:  2 Gaps:  Alignment 799  Matches:  1 Indels:  0 Gaps:
2413 AAAIGGCAAAAGTIGAACAGCCAGIGCCTGAICAITCTGAGCIAGTIGAAGAITCCTCAC 2472  185	2593 TAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGAAAGCCATATT 2652  185	ATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAAACTGAAACTGAAACTGAAATGATTTTCTAAGATGAAGTTCCCTACATTGAAATTATATTTCTAAGGTGAAGTTCCCTACATTGAAATTGAAATTATATTTCTAAGGTGACTTGACCTTGAAGTTCCCACAAAGTTGAAA  TTGCTAATTTCTAAATTAGCCAGGGAATATACTGACCTTGACCTTTTCTAAAGAACTGAAAATTGCCCCAGAAGTTCTTGAAAA  TTGCTAAAGAACATACAACCCAAAGTTGAAGAAAATCACTTGACCTTTTCTAAAAAATGGCCCCATGACCTTTTCTAAAAATGGCTCAAAATTGCCTTCTGTGAAAATTCTAGAAAAAAAA	Validedinalariediniysseraspoludiyisprophergalaryrleudiuser Validedinalariediniysseraspoludiyilililililililililililililililililili

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: SUSANCHION: EXPRESSION
NUMBER OF ENCYDERS: 1508
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
COUNTY: PALO ALTO
COUNTY: PALO ALTO
COUNTY: DALO ALTO
COUNTY: DALO ALTO
COMPUTER: READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: MEDIUM TYPE: Ploppy disk
COMPUTER: MEDIUM TYPE: PLOPPY
SOFTMARE: WOR'D PETECATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
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                                                          US-09-544-776-2 (1-373) x US-09-949-016-3253 (1-1669)
    Indels:
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US-09-023-655-382
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Sequence 3253, Application US/09949016

Releant No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOD1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTHARRE PERSENCE SOURCED OF SEQ ID NOS: 207012

SEQ ID NO 3253

LENGTH: 1669
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                                                                                            108 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC
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ORGANISM: Human
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US-09-949-016-3253
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Matches:
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Mismatches:
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                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 382:
SEQUENCE CHARACTERISTICS:
LENGTH: 2610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LENGTH: LUNGWOT14
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APPLICATION NUMBER PILING DATE:
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Best Local Similarity:
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j Sequence 3309, Application US/USYSSILE
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j GENERAL INFORMATION:
    TITLE OF INVENTER, J Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE REFERENCE: CLOO1307
    CURRENT APPLICATION NUMBER: 60/241,755
    PRIOR APPLICATION NUMBER: 60/231,768
    PRIOR FILING DATE: 2000-10-20
    PRIOR FILING DATE: 2000-90-08
    NUMBER OF SEQ ID NOS: 2000-09-08
    NUMBER OF SEQ ID NOS: 2000-09-08
    NUMBER OF SEQ ID NOS: 2000-09
    TYPE: DNA
    TYPE: DNA
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APPLICANT: VEWTER, J. Craig et al.
APPLICANT: VEWTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHARE: PARESEQ for Windows Version 4.0
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 oAlaPro---AlaProAlaAlaProProSerThrProAlaAlaProLysArgArgGlySe 181
              GAAGCCTGAAGAAGAAGAGTTCCAACCAAAGGCCTGCGGCCACAAAGGGCCCTGGGGCC
                                                               |||||
| TCTAĠĠŤCCTGGCGCCCCCCCCTGTTCTCATAAGCAAAAAGCTATTGACCT
                                                                                                   uLeuTyrTrpArgAspIleLysLysTyrGlyValValPheGlyAlaSerLeuPheLeuLe
                                                                                                               CTCAGCCACCATCAGTTTCCGCATCTAGAAGTCTGTTTTACAAGCAGTGCAGAAAAACCGA
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TCAGAAGTACACGGACTGCCTGCAGTTCTACGTGAACAGCACACTTAAGGAACTGAGGAG
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                                                                                                                                                      uLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLe
                                                                                                                                                                                                       uSerValThrIleSerProArglleTyrLysGlyValIleGlnAlaIleGlnLysSerAs
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; Sequence 1127, Application US/09949016
; Patent No. 6812339
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                                                   rSerGly
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; ORGANISM: Human
US-09-949-016-1127
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R APPLICATION NUMBER: 60/043,580
R PILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,588
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R APPLICATION NUMBER: 60/043,314
R RILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,569
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R APPLICATION NUMBER: 60/047,492
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,598
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,613
R APPLICATION NUMBER: 60/047,613
R APPLICATION NUMBER: 60/047,582
R RILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,612
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,632
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APPLICATION UNMBER: 60/043,669
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,312
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,672
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,315
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APPLICATION NUMBER: 60/056,877
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,889
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,630
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,662
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APPLICATION NUMBER: 60/047,587
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APPLICATION NUMBER: 60/048,974
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/056,886
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APPLICATION NUMBER: 60/056,882
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APPLICATION NUMBER: 60/047,601
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60/047,584
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                                                                                                                                                                                    GLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPh 309
                                    1GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgAr 289
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
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CURRENT PELLING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER PILLING DATE: 1998-03-06
EARLIER PILLING DATE: 1998-03-06
EARLIER FILLING DATE: 1997-03-07
EARLIER PELLING DATE: 1997-05-23
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US-09-149-476-254
; Sequence 254, Application US/09149476
; Patent No. 6420526
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APPLICATION NUMBER: 60/056,884 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/057,669 APPLICATION NUMBER: 60/049,610 FILING DATE: 1997-06-13 APPLICATION NUMBER: 60/061,060 FILING DATE: 1997-10-02 APPLICATION NUMBER: 60/061,060 FILING DATE: 1997-10-02	1.08-3/ Length: 1.08-3/ matches: 153 matches: 153 matches: 153 conservative: 48 Similarity: 44.09% Mismatches: 78 indels: 69 h; Gaps: 9	-544-776-2 (1-373) x US-09-149-476-254 (1-1766)	32 gluaspgluglugluglugluglugluglugluaspgluaspgluaspLeugluglu 51	rAlaAlaPr	TTTCCCC-	ProAlaAlaGlyAlaProLeuMetAspPheGlyAsnAspPheValProProAlaBroArg 91	93TCCCTCTCTCCCCCGTAT 113	92 GlypheLeuproAlaAlaProProValAlaProGluArgGlnProSer 107 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	4 CICIIIICACCCIICCCCACCCICGCGASCAIGGGGGGGGGG	71	128 ValSerProSerLysLeuProGluAspAspGluProProAlaArgProProProProPro 147	192	148 ProAlaSerValSerProGlnAlaGluProValTrpThrProProAlaProAla 167	aProProSerThrProAlaAlaProLysArgArgGlySerSerGlySerValValVal 18	ccacccraggaacaacaaacaa acraccrororororororororororororororororo	leLysLysThrGlyValValPheGlyAlaSe  :::             sTGAAGAACTGGGTTTGTCTTTGGCACCAC	208 LeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAla 227	356 ATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGTTCTTACCTCATCCTGGCT 415	28 LeuleuServalThrIleSerProArgileTyrLysGlyValileGlnAlaileGlnLys 24	16 CTTCTCTCTCTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCTGTACAGAAG 47	rLeuGluSerGluValAlaileSerGluGlu 26	carccartcaaagccractggacgragacartactcrgrccrcagaa 53	G  nLysTyrSerAsnSerA  aLeuG  yHisVa  AsnCysThrI  eLysG  uLeu 28          :::    :::    :::	CTGCCATGGTGCACATCAACAGGGCCCTGAAACTCATT 59	288 ArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 307	
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                                                                                                       GlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGly 367
                                                                                                                                                                                                    328 SerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeu
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
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CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER PELLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER PILLING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/047,600
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,597
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,633
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,492
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 255, Application US/09149476 Patent No. 6420526
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US-09-149-476-255
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R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,582
R FILING DATE: 1997-05-23
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R FLING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,612
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,601
R RILING DATE: 1997-05-23
R RELING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,580
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,586
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,568
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,568
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,314
R FILING DATE: 1997-04-11 R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 66/043,672

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 66/043,315

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/048,974

R FILING DATE: 1997-06-05

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 66/056,895

R FILING DATE: 1997-08-22

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APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,671 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,674 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,911 FILING DATE: 1997-08-22 DATE: 1997-05-23 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/ 1997-08-22 FILING DATE:

MBER: 60 997-08-2 MBER: 60 997-08-2 MBER: 60 997-08-2 MBER: 60 997-08-2 MBER: 60 997-08-2 MBER: 60	1997-08-23 NUMBER: 60/047,595 1997-05-23 NUMBER: 60/047,588 1997-05-23 NUMBER: 60/047,586 1997-05-23 NUMBER: 60/047,586 1997-05-23 NUMBER: 60/047,590 1997-05-23 NUMBER: 60/047,594 1997-05-23 NUMBER: 60/047,594 1997-05-23 NUMBER: 60/047,593 NUMBER: 60/047,593 NUMBER: 60/047,593 NUMBER: 60/047,591 1997-05-23 NUMBER: 60/043,578 1997-05-23 NUMBER: 60/043,576 1997-04-11 NUMBER: 60/043,576 1997-04-11 NUMBER: 60/043,670 1997-04-11 NUMBER: 60/043,670 1997-04-11 NUMBER: 60/056,664 1997-08-22 NUMBER: 60/056,681	MBER: 60 997-08-2 997-08-2 997-08-2 MBER: 60 997-08-2 997-08-2 997-08-2 997-08-2 MBER: 60 997-08-2 MBER: 60 997-08-2 997-08-2
APPLICATION FILING DATE: APPLICATION	100 N 2011 CON 100 N	APPLICATION FILING DATE: APPLICATION
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EARLIER FILING DATE: 1997-10-02	Alignment Scores: 2.42e-36 Length: 2664 Pred. No.: 659.50 Matches: 150 Score: Conservative: 48 Best Local Similarity: 44.51\$ Mismatches: 71 Query Match: 34.53\$ Gaps: 9	(-09-544-776-2 (1-373) x US-09-149-476-255 (1-2664)	42 GluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAlaAla 61	::: 11 GAGCAGAGTAAAGGGACTTGAGCGA	62 GlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAspPhe 81	50 GGATTATTCTCCCC	82 GlyAsnAspPheValProProAlaProArgGlyPheLeuP	68TCCCTCTCTCCCGCCCGTATCTCTTTTCACCCTTCCCCACCTCGCTCG	100ValAlaProGluArgGlnProSerTrpAspProSerProValSerSerThrVal 11	119 CGTASCATGGCGGGGCGTCGGCGGCCA	118 ProAlaProSerPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspAsp 137	138 GluProProAlaArgProProProProProProAlaSerValSerProGlnAlaGluPro 157	:::	158 ValTrpThrProProAlaProAlaProAlaAlaProProSerThrProAlaAlaPro	224	. 178 ArgArgGlySerS	242 AGAGCTGC-AGCTCCTCTGTGCGGTGCACGATCTGATTTTCTGGAGA	198 ThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIle 217	218 ValSerValThrAlaTyrlleAlaLeuAlaLeuLeuSerValThrlleSerProArgil	361 ATCAGTGTGGTTTCTTACCTCAGCTCTTCTCTCTCTGTCACCATCA	238 TyrlysGlyvallleGlnAlalleGlnLysSerAspGluGlyHisProPheArgAlaTyr 25	421 TACAAGTCCGTCATCCAAGCTGTACAGAAGTCAGAAGAAGGCCATCCAT	258 LeuGluSerGluValAlalleSerGluGluLeuValGlnLysTyrSerAsnSerA	481 CIGGACGIAGACATIACTCIGICCICAGAAGCTTTCCATAATTACATGAATGCTGC	278 GlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuVal 29	541 GIGCACATCAACAGGCCCTGAAACTCATTATTCGTCTTTTCTGGT	298 AspS	601 dacrectidaaderoderererardidecreargaeerar	318 GlyLeuThrLeuIeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGlu 3	661 GGAATCACCCTTCTAATTCTTGCTGAACTGCTCATTTCAGTGTCCCGATTGTCTATGAG 72	338 ArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAla 357
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346 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 365
                                                                490 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAACTC 549
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                                                                                                                                                                                                                                                                                               APPLICANT: Bandman, Olga
APPLICANT: Ba-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Halman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
CUTY: COUNTRY: U.S.
ZIP: 94304
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                   366 ProglyLeu---LygArgLygAlaGlu 373
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OPERATING SYSTEM: DOS
SOFTWARE: FRAISEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, LACY J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REJECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-855-0556
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                                                                                                                                                                                                                                   ; Sequence 4, Application US/08700607; Patent No. 5858708; GENERAL INFORMATION:
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INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1095 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER: IBM Compatible
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44.26%
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CLONE: 31870
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Best Local Similari
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Pred. No.:
                                                                                                                                                                                             RESULT 10
US-08-700-607-4
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                                                                                                                                                                             Sequence 2988, Application US/09949016
; Sequence 2988, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT PILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,756
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR PILING DATE: 2000-10-03
CTGCCTCTTCTCTCTCTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCTGTA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 CTGATGATGCTGCTGTTCCTTGATGTTCAGTGTGATGTGTTTCTTACCTCATC 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrlleLys 285
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                                                                358 MetalalysileGlnAlalysIleProGlyLeu---LysArgLysAlaGlu 373
                                                                                      Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2988
LENGTH: 2262
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80.42%
60.32%
32.12%
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Best Local Similarity:
Query Match:
DB:
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3415 AGTATCAGAGAAGCTCCAGGGCAAAAAGCAAGAGGCACCAGACCCAGATGATCATATGT 3474
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CTATGAGAAGTACAAGGATGCACGTGTGCGTAGCGCTGAGCAGGCAAGAGTCCCACACTGA
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                 and
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids and TITLE OF INVENTION: POlypeptides
FILLE OF INVENTION: POlypeptides
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_Ft_genes Version 2.0
SEQ ID NO 111
LENGTH: 3517
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-799-451-111
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Best Local Similarity:
Query Match:
DB:
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               CTCCCGCCCCGTATCTCTTTTTTTTTTTTTTCCCCCTTGCTCGCGTANCATGGCGGAGC 200
                                                                                                                     258 CCGCGCCGGCGGCGGCGGAGCCCAGGAGCCTGCCCCTGGGGA---CGAAGAGCT 314
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                                                           200 ValvalPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSer
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Patent No. 6783969
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Asoundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
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Ma, Yunging
Yamazaki, Victoria
Chen, Rui-hong
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Zhang, Jie
Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
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Wang, Dunrui
Yang, Yonghong
Wehrman, Tom
Ghosh, Reena
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,569
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11

APPLICATION NUMBER: 60/043,671 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,674 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669

APPLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,314

FILING DATE: 1997-04-11 APPLICATION UNMBER: 60/043,312 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,313

FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,672
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,315
FILING DATE: 1997-04-11

FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/056,886

APPLICATION NUMBER: 60/048,974

FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877

FILING DATE: 1997-08-22
APPLICATION UNMBER: 60/056,889
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,893

APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22

FILING DATE: 1997-08-22

APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 ICATION NUMBER: 60/056,662 APPLICATION NUMBER: 60/056,872

FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,882

1997-08-2

FILING DATE:

FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 APPLICATION NUMBER: 60/056,888 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,879 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,880 FILING DATE: 1997-08-22

FILING DATE: 1997-08-2

APPLICATION NUMBER: 60/056,894 APPLICATION NUMBER: 60/056,911 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636

FILING DATE: 1997-08-

APPLICATION NUMBER: 60/056,910

FILING DATE: 1997-08-2

APPLICATION NUMBER: 60, FILING DATE: 1997-08-22

FILING DATE: 1997-08-2

60/056,874

APPLICATION NUMBER: 60/056,845

FILING DATE: 1997-08-2

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APPLICATION NUMBER: 60/056,892
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/057,761
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,631
FILING DATE: 1997-08-22
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3475 TGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAG 3514
                                                                                                                                                    APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/149-476
CURRENT APPLICATION NUMBER: US/09/0493
EARLIER PILING DATE: 1998-09-08
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-05-23
EARLIER PELING DATE: 1997-05-23
EARLIER PILING DATE: 1997-05-23
EARLIER PILIN
                                                                                     ; Sequence 102, Application US/09149476; Patent No. 6420526; GENERAL INPORMATION:
                                          RESULT 12
US-09-149-476-102
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82 59 113 118 152 161

236 198 295 218 353 238

us-09-544-776-2.p2n.rni

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Sequence 1419, Application US/09949016
Batent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REPERENCE: CLOOL307
                                                                                                                                                                                                                                                 AlabroSerPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspAspGlu 138
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EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
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EARLIER PILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/043,576
EARLIER APPLICATION NUMBER: 60/043,670
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EARLIER APPLICATION NUMBER: 60/043,670
EARLIER PILING DATE: 1997-06-22
EARLIER PILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,897
EARLIER PILING DATE: 1997-08-22
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NUMBER: 60/061,060
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GluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAlaAlaGly

US-09-544-776-2 (1-373)

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                      AlaAlaProProSerThrProAlaAlaProLys 177
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPRENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517
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US-09-270-767-13561
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Conservative:
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
SOFTWARE: PASTENCY OF WINDER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASTENCY for WINDOWS VERSION 4.0
SEQ ID NO 1419
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Query Match:
DB:
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ORGANISM: Human
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Pred. No.:
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Sequence 2227, Application US/09513999C

Sequence 2227, Application US/09513999C

SENERAL INFORMATION:

APPLICANT: Dunas Mille Edwards, J.B.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PATENTE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 200-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: PATENT.

LENGTH: 441
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                                                                                                      GlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleVal
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                       US-09-544-776-2 (1-373) x US-09-270-767-13561 (1-2014)
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Pred. No.:
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 Conservative:
Mismatches:
Indels:
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100.00%
18.17%
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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PAT 20-APR-2002
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AX323399 Sequence
AX17810 Sequence
AX17810 Sequence
AX32339 Sequence
AX323392 Sequence
AX3335035 Sequence
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AX537591 Sequence
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AX539587 Sequence
AX337690 Sequence
BD056452 Novel low
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AX53339 Sequence
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Unclassified.
Unclassified.
1 (bases 1 to 48)
Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
Low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis
Atagnosing and treating atherosclerosis
Patent: US 6355451-A 36 12-MAR-2002;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 36 from patent US 6355451.
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AR374696 Sequence
AR409331 Sequence
AX239593 Sequence
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                             nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 50
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DEFINITION ACCESSION VERSION KEYWORDS

RESULT 2 AR374696 LOCUS

SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

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BD056458 10w density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis,.
                                                                                                                                         PAT 26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metacas; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;

Bukaryota; Metacas; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;

1 (bases 1 to 48)

Lees, M.M., Lees, R.S., Law S.W. and Arjona, A.A.

Novel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis

Datent: JP 2001506983-A 16 29-MAY-2001;

BOSTON HEART FOUNDATION INC

PN JP 2001506983-A/16

PP 26-NOV-1997 JP 1998524870

PR 27-NOV-1997 JP 1998524870

PR 27-NOV-1996 US 60/031930,03-JUN-1997 US 60/048547 PI
ANN M LEES, ROBERT S LEES, SINON W LAW, ANIBAL A ARJONA PC

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Low density liprotein binding proteins and their use in diagnosing and treating atherosclerosis
and treating atherosclerosis
Patent: WO 0164874-A 56 07-5EP-2001;
Boston Heart Foundation, Inc. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Matches:
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Mismatches:
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    .48
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 36 from Patent WO0164874.
AX239593
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BD056458.1 GI:22602064
JP 2001506983-A/16.
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Aequorea victoria
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                                                                                                                                                                                                                                                                                                                                                                   Unclassified.

(Decent 1 to 48)

Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.

Low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis

Patent: US 605588-A 36 12-AUG-2003;

Location/Qualifiers
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Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
Leow density lipoprotein binding proteins and their use in
diagnosing and treating atherosclerosis
Patent: US 6632923-A 36 14-OCT-2003;
Location/Qualifiers
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Sequence 36 from patent US 6632923.
AR409331
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Sequence 36 from patent US 6605588.
AR374696
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                          US-09-544-776-2 (1-373) x AR199544 (1-48)
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Query Match: DB:

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PAT 10-MAR-1997
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Crouzet,J., Scherman,D. and Wils,P.
Crouzet,J., Scherman,D. and Wils,P.
DURIPICATION OF A TRIPLE HELIX FORMATION WITH AN IMMOBILIZED
OLIGONUCLEOTIDE
Patent: WO 9618744-A 17 20-JUN-1996;
RHONE POULEMY RORER SA (FR)
Other publication AU 4178996 966703
Other publication FR 2728264 960621.
Location/Qualifiers
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Crouzet, J., Scherman, D. and Wils, P.
Purification of a triple helix formation with an immobilized
oligonuclectide
Patent: US 6287762-A 17 11-SEP-2001;
                                                                                                                                                                                     32 GludspGluGluGluGluGluGluGluGluGludspGludsp 46
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AR167590
AR167590.1 GI:17903379
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Sequence 17 from Patent WO9618744.
A51711
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/organism="unidentified"
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Crouzet, J., Scherman, D., Wils, P., Blanche, F. and Cameron, B.
Purification of a triple helix formation with an immobilized
oligonuclectide
Patent: US 6319672-A 34 20-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crouzet, J., Scherman, D., Wils, P., Blanche, F. and Cameron, B. Purification of a triple helix formation with an immobilized oligonucleotide
Patent: W0 0192511-A 34 06-DEC-2001;
Aventis Pharma (FR)
Location/Qualifiers
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synthetic construct
other sequences; artificial sequences.
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Matches:
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Sequence 34 from patent US 6319672.
AR178317
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Sequence 34 from Patent WO0192511.
AX323399.1 GI:18094161
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AX323399
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Sequence 2153 from patent AR356035 GI:33762119
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AR356035
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Crowlet, J., Scherman, D., Wils, P., Blanche, F. and Cameron, B. Purification of a triple helix formation with an immobilized oligomucleotide
Patent: US 6319672-A 17 20-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B. Purification of a triple helix formation with an immobilized oligonucleotide
Patent: WO 0192511-A 17 06-DEC-2001;
                                                                                                                                                                                    GluAspGluGluGluGluGluGluGluGluGluAspGluAsp 46
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Matches:
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Location/Qualifiers
1. .50
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Sequence 17 from patent US 6319672.
AR178300
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Sequence 17 from Patent WO0192511.
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Location/Qualifiers
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PAT 17-AUG-2003
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Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
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Patent: EP 1281774-A 17 05-FBB-2003;
Aventis Pharma S.A. (FR)
Location/Qualifiers
1. 50
| vorganism="unidentified"
| mol_type="unassigned DNA"
| /db_xref="taxon:32644"
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Staphylococcus aureus polynucleotides and sequences
Patent: US 6593114-A 2153 15-UUL-2003;
Location/Qualifiers
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Sequence 17 from Patent BP1281774.
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Search completed: August 4, 2005, 01:02:09 Job time : 4331 secs
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Unknown.
Unclassified.
1 (bases 1 to 50)
Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and Rosen, C.A.
Staphylococcus aureus polynucleotides and sequences
Patent: US 6737248-A 2153 18-MAY-2004;
Location/Qualifiers
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Sequence 2153 from patent US 6737248.
AR537591. GI:53928808
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Sequence 14 from patent US 6455292.
AR232180. GI:27274071
1. .50
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/organism="unknown"
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143 ProProProProProAlaSerValSerProGlnAlaGluProValTrpThrProPro 162
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Shu,Y., Fan,W., Kovacs,K.F., Zidanic,M. and Jay,G.
Full-length serine protein kinase in brain and pancreas
Patent: US 645522-A 14 24-SEP-2002;
Location/Qualifiers
1. 50
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Matches:
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Abz22092 Polyanion
Adi64451 SSR motif
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Adc56859 Micro gol
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Abs67031 Human MRP
Abx13592 Human ser
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ABK95217
ADK61703
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14-JUL-2000; 2000US-00616289.
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     WO200164874-A2.
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Aas19342 Plasmid X
Abz22128 Polyanion
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(c) 1993 - 2005 Compugen Ltd.
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68
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                                                                       OM protein
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                                                                                                                                                                                  Sequence:
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The present sequence is that of a polynucleotide encoding a fragment of novel low density lipoprotein binding proteins (LBPs) of the invention (see AAB82797-820). LBPs are capable of binding to native and methylated low density lipoproteins (LDLs). Isolated polynucleotides encoding novel LBPs and their fragments are claimed, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is a risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are also claimed, as are pharmaceutical compositions comprising an LBP polypeptide or
                          New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                          as are pharmaceutical compositions compunence or nucleic acid, and vaccine compositions
                                                                                                               Disclosure; Page 10; 143pp; English
                       New isolated low
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Sequence 48 BP; 17 A; 7 C; 24 G; 0 T; 0 U; 0 Other;

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2
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       Length:
Matches:
Conservative:
Mismatches:
                                        Indels:
      4.14e+04
68.00
100.00%
68.75%
3.56%
                                 Similarity:
                       Percent Similarity:
Best Local Similari
Alignment Scores:
                                      Query Match:
DB:
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US-09-544-776-2 (1-373) x AAH26508 (1-48)

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33 AspGluGluGluGluGluGluGluGluGluAspGluAspGluAsp
                                                                  ss; DNA purification; triple helix; plasmid purification.
                                                        (GGA)16 DNA purification oligonucleotide
                            ВР
                           AAS21106 standard; DNA; 48
                                               20-MAR-2002 (first entry)
                                      AAS21106;
                  RESULT 2
                        AAS21106
                            유
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"GAA repeat type" Location/Qualifiers /\*tag= /note= ' repeat\_region repeat\_unit Synthetic.

WO200192511-A2

06-DEC-2001

25-MAY-2001; 2001WO-US017122

26-MAY-2000; 2000US-00580923

(AVET ) AVENTIS PHARMA SA

Cameron D. Blanche Д, Wils Scherman D, WPI; 2002-097772/13. Crouzet J,

Purifying double-stranded (ds) DNA from a solution containing dsDNA and other components, comprises passing the solution through a support comprising a covalently coupled oligonucleotide able to form a triple

Double-stranded (ds) DNA can be purified from complex mixtures of nucleic

Claim 12; Page 25; 34pp; French

of double stranded DNA by triple helix formation - comprises ag immobilised oligo-nucleotide to specific sequence in target

Purificn. of hybridising

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This invention comprises a method of purifying double-stranded DNA from a solution containing the double-stranded DNA mixed with other components, comprising passing the solution through a support comprising a covalently coupled oligonucleotide capable of forming a triple helix with the double stranded DNA by hybridisation with a specific sequence present in the double-stranded DNA. The method is useful for purifying double-stranded DNA contained in a solution and mixed with other components. The new method is a simple, rapid and effective method for DNA purification, and makes it possible to obtain especially high purities with high yields. The method enables DNA to be purified from complex mixtures comprising other nucleic acids, proteins, endocoxins, nucleases and the like. The supports may be readily recycled, and the DNAs obtained display improved properties to pharmaceutical safety. Further, the method entails only one step contrary to prior art. The present sequence represents a DNA sequence contains only interpret sequence contains and purification of the sequence is used for sequence contains the planid pizz752. This sequence is used for
                                                                                                                                                                                                                                                                                                         sequence contained within the plasmid pXL2725. This sequence is used for purification of this plasmid using the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triple helix; triplex formation; Hoogsteen base pairing; plasmid; purification; double-stranded DNA; homopyrimidine; polypurine; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homopurine target for triple helix-forming oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 GluAspGluGluGluGluGluGluGluGluGluAspGluAsp
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                                                                                                                                                                                                                                                                                                                                                               Sequence 48 BP; 16 A; 0 C; 32 G; 0 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                  Example 7; Page 20; 40pp; English
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helix with the dsDNA
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acids, proteins, endotoxins, nucleases, etc. by passing the mixture over a support to which an oligonucleotide is covalently attached; the oligonucleotide is able to form a triple helix by hybridisation with a specific sequence present in the dsDNA. The present sequence is a preferred homopurine target for triplex formation with a single-stranded oligonucleotide. The target sequence may be present naturally, e.g. in a plasmid origin of replication, or can be introduced artificially. The method is particularly suited to purification of plasmid DNA 888888888888

Sequence 50 BP; 17 A; 0 C; 33 G; 0 T; 0 U; 0 Other;

0003750 Conservative: Mismatches: Indels: Length: Matches: Gaps: 66.00 100.00\$ 80.00\$ 3.46\$ 5.27e+04 Similarity: Percent Similarity: Alignment Scores: Best Local S Query Match:

US-09-544-776-2 (1-373) x AAT32776 (1-50)

46 32 GluAspGluGluGluGluGluGluGluGluGluAspGluAsp ò 셤

AAS19342 standard; DNA; 50

BP

AAS19342;

(first entry) 20-MAR-2002

Plasmid XL2725 sequence.

ds; DNA purification; triple helix; plasmid purification; XL27256

Synthetic.

/note= "GGA repeat type" Location/Qualifiers  $/\text{rpt}_{1}^{\perp}\text{type} = \text{TANDEM}_{6}$ ๙ . .50 \*tag= /\*tag= repeat\_region repeat unit 

WO200192511-A2

06-DEC-2001

25-MAY-2001; 2001WO-US017122

26-MAY-2000; 2000US-00580923

(AVET ) AVENTIS PHARMA SA

Cameron B; Blanche F, Crouzet J, Scherman D, Wils P,

WPI; 2002-097772/13.

containing dsDNA and Purifying double-stranded (ds) DNA from a solution containing dsDNA ar other components, comprises passing the solution through a support comprising a covalently coupled oligonucleotide able to form a triple comprising a covalent helix with the dsDNA.

Example 7.1; Page 20; 40pp; English.

This invention comprises a method of purifying double-stranded DNA from a solution containing the double-stranded DNA mixed with other components, comprising passing the solution through a support comprising a covalently coupled oligonucleotide capable of forming a triple helix with the double-stranded DNA by hybridisation with a specific sequence present in the

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double-stranded DNA. The method is useful for purifying double-stranded DNA contained in a solution and mixed with other components. The new method is a simple, rapid and effective method for DNA purification, and makes it possible to obtain especially high purities with high yields. The method enables DNA to be purified from complex mixtures comprising other nucleic acids, proteins, endotoxins, nucleases and the like. The supports may be readily recycled, and the DNAs obtained display improved properties to pharmaceutical safety. Further, the method entails only one step contrary to prior art. The present sequence represents the sequence of the plasmid XL2725 verified upon sequencing, this sequence differs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluAspGluGluGluGluGluGluGluGluAspGluAsp
                                                                                                                                                                                                                                                                                                 0003720
                                                                                                                                                                                                                                        Sequence 50 BP; 17 A; 0 C; 33 G; 0 T; 0 U; 0 Other;
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Mismatches:
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Matches:
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                                                                                                                                                                                                      from the expected sequence (GGA)17
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вР ABZ22128 standard; DNA; 42 ABZ22128; RESULT 

(first entry) 11-MAR-2003

Polyanionic polymer related oligonucleotide #82

Polyanionic polymer; bioactivity; water solubility; ss.

Synthetic

WO200277036-A2.

03-OCT-2002.

21-MAR-2002; 2002WO-US008614.

21-MAR-2001; 2001US-0277705P

(LEUN/) LEUNG D W.

Tompkins CK; Lofquist A, Pietz GE, Bergman PA, Waggoner DW; Leung DW,

WPI; 2003-058367/05.

Producing monodispersed preparation of polyanionic polymer for therapy, by expressing vector comprising ligation product of oligonucleotides encoding glutamate/aspartate residues in host cell and isolating the product

Example 7; Fig 8; 74pp; English.

The present invention describes a method (M) for producing a monodispersed preparation of a polyanionic polymer (PP) larger than 10 kD. (M) involves inserting into an expression vector (EV) a ligation product formed by ligating together oligonuclectides that encode glutamate/aspartate residues, expressing EV in a host cell, and isolating the protein product (P) of EV, where (P) is PP and at least 80% of PP is approximately of the same molecular weight. Also described: (1) a recombinant fusion protein (I) comprising a polyanionic polypeptide and another polypeptide at either one end or at both ends of it; (2) a

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polyanionic polymer (II) conjugate comprising a polyanionic polymer and Leukine, where the polyanionic polymer is polyglutamic acid or polyaparic acid; (3) a vector (III) comprising a cassette which comprises a nuclectide sequence encoding a polyanionic polymer and at least one other nucleotide sequence, where the polyanionic polymer is polyglutamic acid or polyapartic acid; (4) production of (1); (5) a cell (IV) comprising (III) or a vector that comprises a nucleotide sequence that encodes a polyanionic polymer that is larger than 10 kDa; and (6) a recombinantly-produced polyanionic polymer (V) that is of any molecular weight or is larger than 10 kD, and is conjugated to another protein. (I) is useful for treating a disease or ailment in an individual by administering (I) to the individual. (I) is also useful for delivering an effective amount of a pharmaceutically active agent, a therapeutic protein or a drug to a patient in need of it, or for diagnostic and testing or research purposes. AZZ2045 to ABZ2211 and ABB56374 to ABPS6400 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
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BP; 22 A; 0 C; 20 G; 0 T; 0 U; 0 Other; Sequence 42

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                     Conservative:
Mismatches:
Indels:
        Length:
Matches:
                                            Gaps:
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64.00
100.00$
85.71$
3.35$
                      Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                      Query Match:
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US-09-544-776-2 (1-373) x ABZ22128 (1-42)

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GluAspGluGluGluGluGluGluGluGluAspGlu 45
             42
        32
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Polyanionic polymer related oligonucleotide #46.
                                                                                        ABZ22092 standard; DNA; 42
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                                                                                                                                                                                               ABZ22092;
                                    AB2222092

ID AB222092

XX AC AB22

XX 
RESULT 6
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Polyanionic polymer; bioactivity; water solubility; ss.

WO200277036-A2.

21-MAR-2002; 2002WO-US008614. 03-OCT-2002.

21-MAR-2001; 2001US-0277705P.

(LEUN/) LEUNG D W.

Lofquist A, Pietz GE, Tompkins CK; Bergman PA, Leung DW, Be Waggoner DW;

WPI; 2003-058367/05.

Producing monodispersed preparation of polyanionic polymer for theral by expressing vector comprising ligation product of oligonucleotides encoding glutamate/aspartate residues in host cell and isolating the

Disclosure, Fig 5; 74pp; English.

product.

The present invention describes a method (M) for producing a monodispersed preparation of a polyanionic polymer (PP) larger than  $10\,$  kD. (M) involves inserting into an expression vector (EV) a ligation

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product formed by ligating together oligonucleotides that encode glutamate/aspartate residues, expressing EV in a host cell, and isolating the protein product (P) of EV, where (P) is pp and at least 80% of PP is approximately of the same molecular weight. Also described: (1) and control of comprising a polyanionic polypeptide and recombinant fusion protein (I) comprising a polyanionic polypeptide and polyanionic polymer (II) compuser comprising a polyanionic polymer and polyanionic polymer (II) compuser is polyanionic polymer and the polyanionic polymer is polyanionic polymer and at comprises a nucleotide sequence, where the polyanionic polymer is polyanitamic acid or comprises a nucleotide sequence, where the polyanionic polymer is comprises a nucleotide sequence, where the polyanionic polymer is polyglutamic acid or polyapsartic acid; (4) production of [I); (5) a cell (V) comprising (III) or a vector that comprises a nucleotide sequence that encodes a polyanionic polymer (V) that is of any molecular weight or is larger than 10 kD, and is conjugated to another protein. (I) is useful for treating a disease or ailment in an individual by sequence of the individual. (I) is also useful for delivering an effective amount of a patient in need of it, or for diagnostic and testing or research purposes. ABZ22045 to ABZ22131 and ABPS6374 to a testing or research purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP56400 represent sequences used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-544-776-2 (1-373) x ABZ22092 (1-42)
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28-MAR-2000; 2000AU-00006520.
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The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention
                                                                                                                                                                                                                                                                                                                                                            Seguence 45 BP; 0 A; 15 C; 0 G; 30 T; 0 U; 0 Other;
testing the purity of legume seed batches.
                                                  Page 35; 52pp; English.
                                                Claim 6;
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4 4 1 0 0 0 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: 5.88e+04 64.00 100.00\$ 85.71\$ 3.35\$ Similarity: cal Similarity: Alignment Scores: Pred. No.: Query Match: DB: Local

US-09-544-776-2 (1-373) x AAI64451 (1-45)

GluAspGluGluGluGluGluGluGluGluAspGlu 45 32 셤 8

RESULT 8 ADC56858/c

ADC56858;

BP

ADC56858 standard; DNA; 50

(first entry) 18-DEC-2003 Micro gold-electrode DNA chip array oligonucleotide SEQ ID NO 3.

DNA chip; microarray; diagnosis; ss.

Synthetic

JP2003090815-A.

28-MAR-2003

18-SEP-2001; 2001JP-00283412

18-SEP-2001; 2001JP-00283412

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

WPI; 2003-630080/60.

Detecting complementary nucleic acid electrochemically, by immobilizing probe on microelectrode, contacting single-stranded target nucleic acid with probe, and measuring change in oxidation-reduction potential.

Example 1; SEQ ID NO 3; 9pp; Japanese.

The invention relates to detecting a complementary nucleic acid electrochemically, comprising immobilising a probe on a microelectrode, contacting a single-stranded target nucleic acid with the probe, and measuring a change in the oxidation-reduction potential in the microelectrode. The method is useful for detecting a complementary mucleic acid or for disease diagnosis. The method is easy, economical and highly precise. Labeling or modification of the nucleic acid is not required. The method does not require expensive reagents or complicated obseration. The use of the nucleic acid chip reduces the size of the gene diagnosis apparatus making it portable. The present sequence is that of an oligonucleotide probe used in examples of the invention to produce a

0 12 0

Length: Matches: Conservative:

6.46e+04 64.00 42.86%

Percent Similarity:

Alignment Scores:

Pred. No.:

Score:

Sequence 50 BP; 0 A; 50 C; 0 G; 0 T; 0 U; 0 Other;

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The invention relates to detecting a complementary nucleic acid electrochemically, comprising immobilising a probe on a microelectrode, contacting a single-stranded target nucleic acid with the probe, and measuring a change in the oxidation-reduction potential in the microelectrode. The method is useful for detecting a complementary nucleic acid or for disease diagnosis. The method is easy, economical highly precise. Labeling or modification of the nucleic acid is not required. The method does not require expensive reagents or complicated operation. The use of the nucleic acid chip reduces the size of the gene diagnosis apparatus making it portable. The present sequence is that of an oligonuclectide probe used in examples of the invention to produce a micro gold-electrode DNA chip array.
                                                                                                                                                                                                                                    143 ProProProProProAlaSerValSerProGlnAlaGluProValTrpThrProPro 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting complementary nucleic acid electrochemically, by immobilizing probe on microelectrode, contacting single-stranded target nucleic acid with probe, and measuring change in oxidation-reduction potential.
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                                 Sequence 50 BP; 0 A; 0 C; 50 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                   163 AlaProAlaProAlaAlaProPro 170
micro gold-electrode DNA chip array.
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7.16e+04 63.00 46.15\$ 46.15\$

Best Local Similarity:

Query Match:

Score: Percent Similarity:

Indels:

9

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of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM) are considered to the S. aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be obtained. Specifically, sequences which are polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used (and their fragments) are useful as primers or probes for isolating homologues of any of the S. aureus DNA sequences contained on the computer
                                                                                                     ProProProProProAlaSerValSerProGlnAlaGluProValTrpThrProPro 162
                                                                                                                                       -----ccccc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents one of 5191 Staphylococcus aureus DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                    Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide(s) and proteins derived from Staphylococcus aureus -stored on computer readable medium and used in the production of anti-S.aureus vaccines.
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 Local Similarity:
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Sequence 50 BP; 0 A; 46 C; 1 G; 2 T; 0 U; 1 Other;

Alignment Scores:

readable medium

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The invention relates to a multidrug resistance-associated protein 1 (MRP 1) polymucleotide. The polymucleotide is useful in an in vitro method for identifying as single nucleotide polymucphism and for identifying and obtaining a pro-drug or drug capable of modulating the activity of a molecular variant of MRP-1 or for identifying and obtaining an inhibitor of the activity of a molecular variant of MRP-1. The sequences are useful for diagnosing a disorder related to the presence of a molecular variant of MRP-1 or susceptibility to such a disorder, where the disorder is cancer (particularly renal cancer) or a disease related to multidrug
                                                                                                                                      139 ProProAlaArgProProProProProAlaSerValSerProGlnAlaGluProVal 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel multidrug resistance-associated protein 1 polynucleotide useful for diagnosis and treatment of cancer and multidrug resistance related diseases, and for identifying single nucleotide polymorphisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resistance. This sequence represents a human MRP-1 polymorphic DNA region
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112
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                                                                                                        US-09-544-776-2 (1-373) x AAV76464 (1-50)
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The invention relates to a multidrug resistance-associated protein 1 (MRP of identifying as single nucleotide is useful in an in vitro method for identifying as single nucleotide polymorphism and for identifying and obtaining a pro-drug or drug capable of modulating the activity of a molecular variant of MRP-1 or for identifying and obtaining an inhibitor of the activity of a molecular variant of MRP-1. The sequences are useful for diagnosing a disorder related to the presence of a molecular variant of MRP-1 or susceptibility to such a disorder, where the disorder is cancer (particularly renal cancer) or a disease related to multidrug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel multidrug resistance-associated protein 1 polynucleotide useful for diagnosis and treatment of cancer and multidrug resistance related diseases, and for identifying single nucleotide polymorphisms.
                              ProAlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrp 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resistance. This sequence represents a human MRP-1 polymorphic DNA region
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                                                                                                                                                                                                                                                                                                         88; cancer;
                                                                                                                                                                                                                                                                                                      Human; multidrug resistance-associated protein 1; MRP-1;
renal cancer; cytostatic; single nucleotide polymorphism.
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US-09-544-776-2 (1-373) x ABS67031 (1-50)
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ABS67032 standard; DNA; 50
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The invention relates to an isolated polynucleotide (its complement or a sequence 99% similar to it) coding without interruption for a human x88336 polypeptide, a serine protein kinase, comprising the K88336-1 and K88336-2 splice variants appearing as ABG72382 and ABG72383. Also included is a method of identifying an agent that modulates the expression of K88336; and progenitor or pancreas progenitor calls comprising; (a) contacting a cell population comprising the cells with a test agent under conditions effective for the test agent computates the expression of K88336; The polynucleotides are useful as molecular targets or drug targets, and (b) determining if the test agent capent modulates the expression of K88336; The polynucleotides are useful as molecular targets or drug targets, and for detecting, diagnosing, as molecular targets or drug targets, and for detecting, diagnosing, as molecular targets or drug targets, and for detecting, diagnosing, capent modulates prognosticating, preventing or treating diseases or conditions relating to brain and pancreas, such as astrocytoma, melitue 2, helicotid peripapillary chorioretinal degeneration, Beckwith-Miedemann syndrome or congenital hyperinauliniam. The method and polynucleotides are useful in research, diagnosis, drug discovery, therapy, clinical medicine, forensic science and pathology. The gene for K8B336 is located on chromosome lipis. S-pter. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynuclectide coding without interruption for a human KSE336 polypeptide useful for preventing or treating diseases/conditions relating to brain and pancreas, e.g. meningioma, insulin-dependent diabetes mellitus 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; promoter; ds; chromosome 11p15.5-pter; astrocytoma; meningioma; pancreatic adenocarcinoma; insulin-dependent diabetes mellitus 2; helicoid peripapillary chorioretinal degeneration; brain; pancreas; Beckwith-Wiedemann syndrome; congenital hyperinsulinism; KSE336.
                                                                                                                                                                                                                                                                                                                                                                                   Human serine protein kinase KSE336 promoter fragment #8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-2002
                                       21
                                                                                                                                                                                                                                               ABX13592;
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DB:
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143 ProProProProProAlaSerValSerProGlnAlaGluProValTrpThrProPro 162

163 AlaProAlaProAlaAla 168

8 8

42 CCGCCGCCGCCGCCGCCG

18 AGGCCGCGCCCCGCGC 1

224

Mismatches: Indels:

46.15% 3.14% 10

Best Local Similarity:

Query Match: DB:

Gaps:

(1-50)

US-09-544-776-2 (1-373) x AAD60995

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The present invention relates to KSE336 polynucleotides encoding serine/
threonine kinase (STK) proteins. Sequences of the invention are useful
tor diagnoshing a brain or pancreas disease associated with abnormal
KSE336, or susceptibility to the disease. They are useful for assessing a
therapeutic or preventative intervention in a subject having a brain or
pancreas disease. The invention is useful for identifying an agent that
modulates the expression of KSE336 in brain or pancreas cells, cells
derived from brain and pancreas or brain and pancreas progenitor cells.
It is useful for detecting polymorphisms in KSE336. It is also useful for
advertising KSE336 for sale, commercial use or licensing. KSE336
sequences are useful to treat diseases such as astrocytoms, meningioma,
pancreatic adenocarcinoma, insulin-dependent diabetes mellitus, Beckwith-
Wiedemann syndrome or congenital hyperinsulinism. They are also useful in
143 ProProProProProAlaSerValSerProGlnAlaGluProValTrpThrProPro 162
                                                                                                                                                                                                                                                                                                                                          brain disease; astrocytoma; meningioma; pancreatic adenocarcinoma; insulin-dependent diabetes mellitus; Beckwith-Wiedemann syndrome; congenital hyperinsulinism; immunotherapy; immunosuppressive; cytostatic;
                                   ------ccccc 19
                                                                                                                                                                                                                                                                                                                           Human, KSE336 protein, serine/threonine kinase, STK, pancreas disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated KSE336 polynucleotide useful for treating meningioma pancreatic adenocarcinoma, helicoid peripapillary chorioretinal degeneration, insulin-dependent diabetes mellitus 2, and congenital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunotherapy. The present sequence is human KSE336 promoter DNA
                                                                                                                                                                                                                                                                                       Human serine/threonine kinase KSE336 promoter DNA #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 2 A; 17 C; 30 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fan W, Kovacs KF, Zidanic M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 19; Opp, English.
                    42 CCGCCGCCGCCGCCGCCG----4
                                                                      163 AlaProAlaProAlaAla 168
                                                                                                                                                                                 ВЪ.
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                                                                                                          18 AGGCCCGCCCCCGCGCC
                                                                                                                                                                               AAD60995 standard; DNA; 50
                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHU Y.
FAN W.
KOVACS K F.
ZIDANIC M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-765475/72
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                                                                                                                                                                                                                AAD60995;
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(ZIDA/) ;
(JAYG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SHUY/)
(FANW/)
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                                                                                                                                           RESULT 14
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This invention relates to a novel isolated serine protein kinase polymucleotide KSE336 exhibiting serine or threonine kinase activity, coding without interruption a fully defined sequence of 668 amino acids or 585 amino acids as given in the specification. The invention may be useful for the development of compounds with an antidiabetic activity or for use in gene therapy, a vaccine or immunotherapy. The invention is useful for diagnosing a brain or pancreas disease associated with abnormal KSE336, or susceptibility to the disease, which involves assessing the expression of the nucleotide of the invention in a tissue pancreas or brain, and comparing the expression to the expression of the gence of a known normal tissue. The disease is astrocytoma, meningioma, gene of a known normal tissue. The disease is astrocytoma, meningioma, wiedemann syndrome or congenital hyperineulinaemia. The present sequence is a human KSE336 promoter sequence which is related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated serine protein kinase polynucleotide KSE336 present in brain and pancreas, and exhibiting serine or threonine activity, useful for diagnosing and treating diseases related brain and pancreas.
                                                                                                                                                                                                                   Beckwith-Wiedemann syndrome; congenital hyperinsulinaemia; promoter; ds;
                                                                                                                                                          antidiabetic; gene therapy; vaccine; immunotherapy; brain disease; pancreas disease; pancreas cell; brain cell; astrocytoma; meningioma; pancreatic adenocarcinoma; insulin-dependent diabetes mellitus;
                                                                                                                                            serine protein kinase; KSE336; serine kinase; threonine kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jay
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                                                                                                          Human KSE336 promoter sequence SegID14.
BP
                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2002; 2002US-00195071.
                                                                                                                                                                                                                                                                                                                                                                                                                     16-AUG-2001; 2001US-00930181.
ADH59088 standard; DNA; 50
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-118904/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIDANIC M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ZIDA/) ZIDANI
(JAYG/) JAY G.
                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                        25-MAR-2004
                                                                                                                                                                                                                                                                                                                                             22-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                    ADH59088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHUY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FANW/)
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0 120

Length: Matches: Conservative:

9.67e+04 60.00 46.15%

Percent Similarity:

Alignment Scores:

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175 0 750
XX
SQ Sequence 50 BP; 2 A; 17 C; 30 G; 1 T; 0 U; 0 Other;
                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                             9.67e+04
60.00
46.15%
46.15%
3.14%
                     Alignment Scores:
Pred. No.:
Score:
Percent Similarity: 4
Query Match: 1
DB:
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US-09-544-776-2 (1-373) x ADHS9088 (1-50)

Search completed: August 4, 2005, 01:11:41 Job time : 563 secs

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1M0532M11

T. brucei df09f10.w tg94g02.b

1M0100N08

2M0033006 2M0085K24

2M0168A19 2M0238F20

Reverse B Forward B Reverse B

Forward Reverse

OM protein

Run on:

Sequence:

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EST 11-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 49)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mr62a06.rl Stratagene mouse testis (#937308) Mus musculus CDNA clone IMAGE:602002 5' similar to TR:G307311 G307311 HISTONE H4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mary Mydouse EST Project
Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                        AZ506149
AZ7656875
AZ7658875
AZ76388
AZ773388
BL491464
CV304274
CV304274
CV304274
AZ56097
AZ56166
AZ816162
AZ86162
AZ816129
CR025955
CR031825
CR031825
CR085382
CR162612
CR162612
CR162612
AZ816212
AZ816212
AZ816213
AZ826179
AZ82657
AZ826577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Possible reversed clone: similarity on wrong strand
Seg primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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              AZ646447
AZ506149
AZ656875
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AZ342202
AZ981881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
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AUTHORS
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KEYWORDS
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-MODEL=frame+_p2n.model -DEV=x1p
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CG731182 1119136A0
AZ840678 2M0138016
CR041958 Porward s
AZ861612 2M0168P16
AL75252 Arabidops
BX002655 Arabidops
                                                                                       August 3, 2005, 17:14:22 ; Search time 3086 Seconds (without alignments) 4600.769 Million cell updates/sec
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1 MEDLDQSPLVSSSDSPPRPQ.....VKDAMAKIQAKIPGLKRKAE 373
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              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                  - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                   34239544 segs, 19032134700 residues
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Maximum Match 100%
Listing first 45 summaries
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T. brucei 1M0075G11 1M0065A01 2M0101A07

ul68c04.v

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 05-JUL-2004
                                                                                                                              BX976589 50 bp DNA linear GSS 05-JUL-200 Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN304a05, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      189 LeuLeuTyrTrpArgAsplleLysLysThrGlyValValPheGly 203
                                                                                                                                                                                                                                                                                                                                                                                                                    32 GluAspGluGluGluGluGluGluGluGluGluAspGluAsp 46
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Location/Qualifiers
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/clone_lib="MHPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BX976589.1 GI:49708012
                                                                                                                                                                                                                                                                                2.11e+04
70.00
93.33%
73.33%
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70.00
100.00%
86.67%
3.66%
                                                                                                         /sex="males"
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                                                                                                                       /tissue
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             FEATURES
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/db xref="taxxon:4577"
//tisue type="leaf"
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//dev_stage="leaf"
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//dev_stage="leaf"
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//dof_elib="lil9" - RescueMu Grid AA"
//dof_elib="load.bone") Site 1: BamHI; Site 2: BglII;
//designed to allow plasmid rescue from total genomic DNA.
//designed to allow plasmid rescue from total genomic DNA.
//designed to allow preferentially into transcription
//designed to allow preferentially into transcription
//designed to file AA was grown at UC San Diego in 2002. DNA
//descueMu. Grid AA was grown at UC San Diego in 2002. DNA
//descueMu. Grid AA was grown at UC San Diego in 2002.
//dever transformed and then screened on LB
//dever transformed and then screened on LB
CG731182 50-OCT-2003
1119136A08.y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
                                                                                                                                                                                                                                                                                                                                                   Waize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Tel: 650 725 2221
Email: walbot@stanford.edu
Plate: 1119136 row: A column: 08
                                                                                                                                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 50)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: transposon-tagged.
Location/Qualifiers
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GSS.
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46.43%
46.43%
3.56%
                                                      survey sequence.
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REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

ACCESSION

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GR041958.1 GI:49775013
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 50)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J., and Bradley, A.
                                                                                                                 CR041958 S5-JUL-2004 Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP150e03, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. http://www.sanger.ac.uk/MICER
Location/Qualifiers
  1. .50
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
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AZ861612
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarese gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AP129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xil0-Gold (Stratagene) cells
and selected for ampicillin resistance."
AZ840678 1inear GSS 20-FEB-2001 2M0138016F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0138016 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                             Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 49)

Dunn, D., Aoyagi, Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Menen, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Miderhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0003
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror:
Plate: 0138 row: O column: 16
Seg primer: CGTYGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="UUGC2M0138016"
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Location/Qualifiers
                                                                                       AZ840678.1 GI:13010586
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100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
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FEATURES

Conservative: Mismatches: Indels: Length: Matches:

Gaps:

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AZ861612
2M0168P16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0168P16 F, genomic survey sequence.
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nederhausern, A. and Wright, D., Weise, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb
143 ProProProProProAlaSerValSerProGlnAlaGluProValTrpThrProPro 162
                                                                 ------ccccc 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                         163 AlaProAlaProAlaAlaProPro 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
Mus musculus
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US-09-544-776-2 (1-373) x AZ840678 (1-49)

ORIGIN

Score:

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Submitted (31-MRR-2004) Weisshaar B., Max-Planck-Institut fuer Submitted (31-MRR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the right border of the T-DNA. Details on the protocols used for generation of the sequence are described in References 1.3. Re-examination of the source from which this sequence has been produced indicates that the sequence is of low reliability. Therefore, no information on a potential insertion site is deduced. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI-Kat information on line availability can be found at: location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC106 (GenBank accession number: AJ537513). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequence to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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                                                                  Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 ProProProProProAlaSerValSerProGlnAlaGluProValTrpThrProPro 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="GK-014A05-012792"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                            Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
                                                                                                                                                                                                                                                                                                                              High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B. Direct Submission
                                                                                                                                               flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
14756321
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/mol_type="genomic DNA"
/strain="Columbia 0"
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                       12874060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwayed (gql 4732114|gbl A7129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL752522 48 bp DNA linear GSS 31-MAR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-014A05-012792,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0168 row: P column: 16
Seq primer: CGTGTAAAACGACGCCAGT
Class: plaemid ends
High quality sequence stop: 31.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC2M0168P16"
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                     Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity:
Query Match:
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Strizhov, N., Li, Y., Rosso, M.G. and Weisshaar, B.

Strizhov, N., Li, Y., Rosso, M.G. and Weisshaar, B.

Direct Submission

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
Details on the protocols used for generation of the sequence are
described in References 1-3. Re-examination of the source from
which this sequence has been produced indicates that the sequence
is of low reliability. Therefore, no information on a potential
insertion site is deduced. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
Location/Qualifiers
                                                                                                                                     An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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Reverse strand read from insert in 3'HPRT insertion targeting and
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/clone="GK-366A11-017045"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                       Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
                                                                                                                                                                                                                                                                                                                                                   High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
                                                                                                     Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weisshaar, B.
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/mol_type="genomic DNA"
/strain="Columbia 0"
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Mismatches:
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     Bioinformatics 19 (11), 1441-1442 (2003)
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                                                                                                                                          Trypanosoma Lorday, Almeropiasitida; Irypanosomatidae; Trypanosoma, S., Ennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Nobmitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

Combridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREB1927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.cg

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX002655 50 bp DNA linear GSS 01-APR-2004 Arabidopsis thaliana T-DNA flanking sequence GK-366All-017045, genomic survey sequence.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
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                                                                                                                             Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="33d12"
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                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 50)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Adams, D.J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.
Direct Submission
Submitted (D. FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. http://www.sanger.ac.uk/MICER
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Miederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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chromosome engineering clone MHPP120c05, genomic survey sequence.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Insert Length: 10000 Std Error: 0.00
Plate: 0512 row: A column: 06
Seg primer: CACACAGGAAACAGCTATGACC
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CRIS4670.1 GI:49933515
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
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/clone="MHPP120c05"
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAD42 (gil-4732114[gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xillo-Gold (stratagene) cells and selected for ampicillin resistance."
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Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Nese,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weise,R.
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1M0347J05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0347J05 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                  /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Twetcor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/64 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Unpublished (2006)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                       'mol_type="genomic DNA"
'strain="C57BL/6J"
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                                                                                                                                                                                                            clone="UUGC1M0512A06"
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High quality sequence stop: 4
Location/Qualifiers
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Mus musculus
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/ Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ clone lib="Mouse 10kb plasmid UUGCIM library"
/ clone lib="Wouse 10kb plasmid UUGCIM library"
/ note="WetCor: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse one
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Resear
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gex="Male"
// Jab hose="B. Coli strain XL10-Gold, T1-resistant, F-"
// Jab hose="B. Coli strain XL10-Gold, T1-resistant, F-"
// Clone lib="Wouse 10kb plasmid UUGCIN library"
// note="Wouse 10kb plasmid UUGCIN library"
// note="Wouse DAN Resource
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gel 4732114|gbh AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xili0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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AZ656875
AZ656875.1 GI:11794021
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musina
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Matches:
Conservative:
Mismatches:
                         Rm. 308, Biomedical Polymers Research Bld 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu nisert Length: 10000 Std Error: 0.00 Plate: 0347 row: J column: 05 Seq primer: CGTTGTAAAACGACGGCCAGT Class: plasmid ends High quality sequence stop: 49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
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KEYWORDS
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

CCESSION

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163 AlaProAlaProAlaAlaProPro 170
                                                                   25 cccccccccccccccccccccccc
                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                                             AZ773388.1 GI:12897698
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64.00
42.86%
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Fax: 801 585 7177
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SOURCE
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                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 49)
Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                              plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XLI0-Gold, Tl-resistant, F-" /clone_lib=Mouse_l0kb plasmid UUGCIM library" /note="Vector: FWD42rv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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Matches:
Conservative:
Mismatches:
Indels:
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0560 row: O column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .49
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/sex="Male"
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Location/Qualifiers
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                                                                                           Mus musculus (house mouse)
                        AZ764533.1 GI:12879593
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DB:
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.. No.:

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/sex="Male" Coll strain XLIO-Gold, Tl-resistant, F-"
/lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
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/note="Vector: PWDAJUN; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
/clone library li
149 bp DNA linear GSS 16-FEB-2001 1M0584E23R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0584E23 R, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamaalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 49)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             947
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Insert Length: 10000 Std Brror: 0.00
Plate: 0584 row: E column: 23
Seg primer: CACACAGGAAACAGCTATGACC
Class: plaemid ends
High quality sequence stop: 49.
Location/Qualifiers
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/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Best Local Similarity:	Query Match:	DB:

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1 17		GlnAlaGluPro	
Gaps:	3 (1-49)	laSerValSerPro	
en n n 0	US-09-544-776-2 (1-373) x AZ773388 (1-49)	ProProProProProProAlaSer	
DB:	US-09-544-776-2	Qy 143 P	

Search completed: August 4, 2005, 02:03:21 Job time : 3091 seca

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BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND TREATING ATHEROSCLEROSIS
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COMBUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-UNN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arjona, Anthal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
                                                                                                                                                                        US-08-068-747-4
US-09-083-123-2
US-09-083-123-8
US-08-589-109A-12
US-09-083-123-4
                                          US-09-580-923-34
US-09-119-507B-78
US-08-897-556A-78
US-09-547-693-78
                                                                                                               US-09-119-507B-88
US-08-897-556A-88
US-09-547-693-88
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US-09-590-211A-5
                                 JS-09-590-211A-9
                                                                                         US-08-860-038-17
US-09-580-923-17
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                                                                                                                                                   US-08-068-747-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36, Application US/08979608A Patent No. 6355451
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston STATE: MA
US-08-979-608A-36
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                                                                                                                                                                                                                                                                                                                                                                         Command line parameters:
-MODEL=frame+ p2n. model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_D_VIS09544776/runat_03082005_181415_27646/app_query.fasta_1.519
-Q=/cgn2_1/USPTO_spool_D_VIS09544776/runat_03082005_181415_27646/app_query.fasta_1.519
-D=18elseued_Patente NA -OFMT=fastap -SUPFIX=p2ns21m50.rni -MINMATCH=0.1
-LOOPENX=0 -LOOPENX=0 -UNITS=bits -START=1 -END=-1 -MATRIX=b10sum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=200 -NORM=ext -HEAPSIZE=500 -MINLEN=0
-TRANS=NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAROP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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36, Appl
34, Appl
17, Appl
2153, Ap
2153, Ap
14, Appl
30, Appl
30, Appl
                                                                          August 3, 2005, 17:14:22; Search time 206 Seconds (without alignments) 2962.773 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34, A
Sequence 17, A
Sequence 17, A
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Sequence 30,
                                                                                                                                                  MEDLDQSPLVSSSDSPPRPQ.........VKDAMAKIQAKIPGLKRKAE 373
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1: /cgn2_6/ptodatcal/ina/5A_COMB.seq:*
/cgn2_6/ptodatcal/ina/5B_COMB.seq:*
3: /cgn2_6/ptodatcal/ina/6A_COMB.seq:*
/cgn2_6/ptodatcal/ina/6B_COMB.seq:*
5: /cgn2_6/ptodatcal/ina/pcruck_COMB.seq:*
6: /cgn2_6/ptodatcal/ina/pcruck_COMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                       nucleic search, using frame_plus_p2n model
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US-09-517-849-36
US-09-616-289-36
US-09-580-923-34
US-09-580-923-17
US-09-95-17-2153
US-08-781-986A-2153
US-08-939-181-14
US-09-930-181-14
US-09-910-181-14
US-09-517-849-30
US-09-517-849-30
                                                                                                                                                                                                                                                                    of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Ygapext
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Ygapop 10.0 ,
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Match
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Perfect score:
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Result No.

Total number

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US-09-544-776-2 (1-373) x US-09-616-289-36 (1-48)
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                                      NAME/KEY: Coding Sequence
LOCATION: 1...48
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36, Application US/09616289
Patent No. 6632923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 34, Application US/09580923; Patent No. 6119672; GANEAL INFORMATION: APPLICANT: Crouzet, Joel; APPLICANT: Scherman, Daniel
                                                                                                                                                                  68.00
100.00%
68.75%
3.56%
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100.00$
68.75$
3.56$
     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-616-289-36
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Pred. No.:
                     FEATURE:
                                                                                           US-09-517-849-36
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US-09-580-923-34
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
   TELEPHONE: 617/542-5070
   TELEFRAX: 617/542-5070
   TELEFAX: 617/542-8906
   INFORMATION FOR SEQ ID NO: 36:
   SEQUENCE CHARACTERISTICS:
   LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 AspGluGluGluGluGluGluGluGluGluAspGluAspGluAsp 48
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OPERATING SYSTEM: DOS
SOFTWARE: FASTESE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION NUMBER: 35,965
REGISTRANCE/DOCKET NUMBER: 10797-003001
TELECOMMULICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-544-776-2 (1-373) x US-08-979-608A-36 (1-48)
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                                                                                                                                                                                                     NAME/KEY: Coding Sequence
LOCATION: 1...48
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish & Richardso
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36, Application US/09517849
Patent No. 6605588
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Ann M.
Lees, Ann M.
Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READALLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO. 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                               68.00
100.00%
68.75%
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                                                                                                                                                                                                                                                                                                                                                                                       .56%
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Best Local Similarity:
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                                                                                                                                                                                     FEATURE
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DB:
                                                                                                                                                                                                                                                                                                                  No.:
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PATCHIANT LEES, AUN M.
APPLICANT: Lees, AUN M.
APPLICANT: Lees, AUN M.
APPLICANT: Lees, Simon W.
APPLICANT: Lees, Simon W.
APPLICANT: Lees, Simon W.
APPLICANT: Lees, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REPRENCE: 10797-004001
CURRENT APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR PLING DATE: 2000-03-02
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-10-30
PRIOR FILING DATE: 1997-10-30
PRIOR FILING DATE: 1997-10-30
PRIOR FILING DATE: 1997-10-30
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFURARE: FEALESQ for Windows Version 4.0
SEQ ID NO 36
                                                                                                                                                               48
                                                                                                                                                                                    33 AspGluGluGluGluGluGluGluGluGluGluAspGluAspGluAsp
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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Conservative:
Mismatches:
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Sequence 17, Application US/09580923

Sequence 17, Application US/09580923

Sequence 17, Application US/09580923

GENERAL INFORMATION:

APPLICANT: Crouzet, Joel

APPLICANT: Cameron, Beatrice

APPLICANT: Wils, Pierre

APPLICANT: Wals, Pierre

APPLICANT: Manche, Francis

TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE

FILE REFRENCE: 03804.0138-01

CURRENT APPLICATION NUMBER: US/09/580,923

CURRENT PILING DATE: 1997-06-09

PRIOR FILING DATE: 1997-06-09

PRIOR FILING DATE: 1995-11-08

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 17

LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 GluAspGluGluGluGluGluGluGluGluGluAspGluAsp 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-580-923-17
                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEPAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: other nucleic acid
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-544-776-2 (1-373) x US-08-860-038-17 (1-50)
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Matches:
    REFERENCE/DOCKET NUMBER: ST94090-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                         1.29e+03
66.00
100.00%
80.00%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
        APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Francis
TITLE OF INVENTION: PURITION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: PURITION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: PURPERSINES: US/09/580,923
CURRENT APPLICATION NUMBER: US/09/580,923
CURRENT PILING DATE: 2000-05-26
PRIOR FILING DATE: 1997-06-09
PRIOR FILING DATE: 1997-06-09
PRIOR PLILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: PCT/FR95/01468
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 34
LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/08860038
Patent No. 6287762
GENERAL INFORMATION:
APPLICANT: SCHERMAN, Daniel
APPLICANT: SCHERMAN, Daniel
TITLE OF INVENTION: FURIFICATION OF A TRIPLE HELIX FORMATION
TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE
NUMBER OF SEGURGES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 GluAspGluGluGluGluGluGluGluGluGluAspGluAsp 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: oligonucleotide
US-09-580-923-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 7 F O O O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-544-776-2 (1-373) x US-09-580-923-34 (1-48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indel8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: FR 94/15162
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR95/01468
FILING DATE: 08-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Savitzky Esq., Martin F. REGISTRATION NUMBER: 29,699
                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.23e+03
66.00
100.00%
80.00%
Wils, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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US-08-860-038-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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000372

46

00 3 7 2 0

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TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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TOPOLOGY: lir
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                                                                                                                                    Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 ProProAlaArgProProProProProAlaSerValSerProGlnAlaGluProVal 158
                                                                                                                                                                                                                                                                                                                               COUNTRY: User
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: JO-Oct-1997
CLASSIPICATION: UNMBER: 60/09,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: 46,789
REFERENCE/DOCKET NUMBER: 98248P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-544-776-2 (1-373) x US-08-956-171E-2153 (1-50)
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Matches:
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SEQUENCE DESCRIPTION: SEQ ID NO: 2153:
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US-08-781-986A-2153
; Sequence 2153, Application US/08781986A
; Patent No. 6737248
; Patent No. 6737248
; GENERAL INFORMATION:
APPLICANT: Charles Kunsch
            Sequence 2153, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2153:
SEQUENCE CHARACTERISTICS:
                                                                                                 Gil H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 TrpThrProProAlaPro 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.08e+03
63.00
46.15%
46.15%
3.30%
                                                                                                                                                                                                                                                                                                                   STATE: Maryland COUNTRY: USA
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Best Local Similarity:
Query Match:
DB:
US-08-956-171E-2153
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US-09-930-181-14/c
US-09-930-181-14/c
Sequence 14, Application US/09930181
Patent No. 645592
GENERAL INFORMATION:
APPLICANT: Origene Technologies
TILE REPERENCE: 160 101 VI
FILE REPERENCE: 160 101 VI
CURRENT APPLICATION WUMBER: US/09/930,181
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 ProproAlaArgProProProProProAlaSerValSerProGlnAlaGluProVal 158
IIILE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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Conservative:
Mismatches:
Indels:
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                    NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS: SCIENCES, INC.
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
STRYE: Rockville
STATE: Maryland
COUNTRY: USA
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                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                              ATFILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: 98248P)
TELECOMMUNICATION INFORMATION:
TELEFARA: (301) 309-8512
TELEFARA: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2153: SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 TrpThrProProAlaPro 164
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46.15%
46.15%
3.30%
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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THEIR USES IN DIAGNOSING AND
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                                                                                                                            34 GluGluGluGluGluGluGluGluAspGluAspGluAsp
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 0 0 0 0 0
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                     BINDING PROTEINS AND THE TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Myers, Louis
REGISTRATION UNDER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
   Mismatches:
Indels:
Gaps:
                                                                       US-09-544-776-2 (1-373) x US-08-979-608A-30 (1-45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-544-776-2 (1-373) x US-09-517-849-30 (1-45)
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1...45
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coding Sequence
                                                                                                                                                                                          US-09-517-849-30
; Sequence 30, Application US/09517849
; Patent No. 6605588
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                 APPLICANT: Lees, Ann M.
Lees, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.438+03
59.00
100.00%
60.00%
3.09%
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                                                                                                                                                                                                                                                                                                    Law, Simon W.
   3.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
     Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
Query Match:
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                    Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
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                                                                                                                                                           143 ProProProProProAlaSerValSerProGlnAlaGluProValTrpThrProPro 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myes, Louis
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 35,965
TELCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

ZIP: 02110-2804

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEG for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 26-No. 6355451-1997

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Arjona, Anibal A. TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
   12 0 12 11 12 1
Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
                                                                                                                        US-09-544-776-2 (1-373) x US-09-930-181-14 (1-50)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1...45
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 225 Franklin Street
CITY: Boston
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                                                                                                                                                                                                                                                                                                                                 Sequence 30, Application US/08979608A Patent No. 6355451 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 617/542-5070
                                                                                                                                                                                                                            163 AlaProAlaProAlaAla 168
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617/542-8906
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                                                                                                                                                                                                                                                               18 AGGCCCCCCCCCCCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 30
SEQUENCE CHARACTERISTICS
 3.36e+03
60.00
46.15%
46.15%
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59.00
100.00%
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish &
                                                                   .14%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MA
                                  Percent Similarity:
Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEATURE
                                                                   Query Match:
DB:
 Pred. No.:
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Score:
                    Sequence 30, Application US/09616289
Fatent No. 6632923
GENERAL INFORMATION
APPLICANT: Lees, Ann M.
APPLICANT: Arjona M.
AP
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Patent No. 5674687

GENERAL INFORMATION:
APPLICANT: Hershfield, Bennett
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 GluGluGluGluGluGluGluGluGluAspGluAspGluAsp 48
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ZIP: 14603
MEDIUM TYPE: Ploppy disk
COMPUTER IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/563,864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.43e+03
59.00
100.00%
60.00%
3.09%
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CORGANISM: Homo sapiens
US-09-616-289-30
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Best Local Similarity:
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US-09-616-289-30
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US-08-563-864-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
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Sequence 1, Application PC/TUS9506839
Sequence 1, Application PC/TUS9506839
Sequence 1, Application:
APPLICANT: Hershfield, Bennett
TITLE OF INVENTION: A METHOD FOR THE IDENTIFICATION
TITLE OF INVENTION: OF NUCLEIC ACID SAMPLES FROM DNA-CONTAINING ORGANISMS NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSES: Nixon, Hargrave, Devans & Doyle
STRRET: Clinton Square, P.O. Box 1051
CITY: Rochester
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                        8 60 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: PREPRING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 AspGluProProAlaArgProProProProPro 148
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Goldman Esq., Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/COCKET NUMBER: 19603/160 (D-1452)
TELECHMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Goldman Esg., Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/160 (D-1452)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-544-776-2 (1-373) x US-08-563-864-1 (1-38)
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,395
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (716) 263-1304
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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75.00%
75.00%
3.04%
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE: NO US-08-563-864-1
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Pred. No.:
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Sequence 9, Application US/08068747

Patent No. 5695933

GENERAL INFORMATION:
APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Housman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
TITLE OF SEQUENCES: 11

CORRESPONDENCES: 11

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massacnusett
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIPICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Granahan Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 31,227
RELEPAK: 617-661-6540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TTELEPAK: nucleic acid
STRANDBNESS: single
TTELOGOCY: linear
TOPIC/CY: linear
TOPIC/CY: linear
TOPIC/CY: linear
TOPIC/CY: linear
TOPIC/CY: linear
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STREET: Two Militia Drive
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60000
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                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic"
 DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.91e+03
57.00
100.00%
91.67%
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75.00%
75.00%
3.04%
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STATE: Massachusett
                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
) MOLECULE TYPE:

) HYPOTHETICAL: N

; ANTI-SENSE: NO

PCT-US95-06839-1
                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-08-068-747-9/c
                                                                                         Alignment Scores:
Pred. No.:
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DB:
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1p
-MODEL=frame+ p2n.model -DEV=x1p
-Q=/cgn2 1/USPTO spool p/US09544776/runat_03082005_181415_27663/app_query.fasta_1.519
-Q=/cgn2 1/USPTO spool p/US09544776/runat_03082005_181415_27663/app_query.fasta_1.519
-D=Published Applications NA -QFMT=fastap -SUFFIX=p2ns21m50.rmp
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRX.Falosum62 -TRAMS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAFSIZE=500 -MINIEN=0 -MAXLEN=50
-USRE=USO9544776 @CGN 1 1 723 @runat 03082005 181415_27663 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 .XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOPE -DBLEXT=7
                                                                                          August 3, 2005, 17:14:22 ; Search time 686 Seconds (without alignments) 3519.226 Million cell updates/sec
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| Published Applications NA:*
| Can2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| Can2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
| Can2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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| Can2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| Can2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| Can2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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| Can2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| Can2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| Can2_6/ptodata/2/pubpna/USO9_REW PUB.seq:*
| Can2_6/ptodata/2/pubpna/USO9_REW PUB.seq:*
| Can2_6/ptodata/2/pubpna/USO9_REW PUB.seq:*
| Can2_6/ptodata/2/pubpna/USO9_REW PUB.seq:*
| Can2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
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1 MEDLDQSPLVSSSDSPPRPQ......VKDAMAKIQAKIPGLKRKAE 373
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:
OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                           US-09-544-776-2
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Maximum DB seg length: 50
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                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1

15-09-962-055-36

Sequence 36, Application US/09962055

Patent No. US20020052033A1

GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Law, Simon W.
Arjona, Anibal A.

Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

TREATING PROTEINS AND THEIR USES IN DIAGNOSING ANI
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:

Annurssee: Fish & Richardson P.C.

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Score:
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Sequence 36, Application US/09976740

Sequence 36, Application US/09976740

GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 1077-004001

CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-27

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1997-11-27

PRIOR APPLICATION NUMBER: US 60/031,930
                                                                                                                                                                                                                                                                                                                                                                               NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERIGICS:
LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 AspGluGluGluGluGluGluGluGluGluAspGluAspGluAsp 48
                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: FRASEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Coding Sequence
LOCATION: 1...48
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
225 Franklin Street
                                                    COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429
68.00
100.00%
68.75%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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Best Local Similarity:
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So
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GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REPERENCE: 10797-004001

CURRENT FILING DATE: 2000-01-12-17

PRIOR FILING DATE: 2000-07-14

PRIOR PELICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR PELING DATE: 1997-11-26

PRIOR PILING DATE: 1997-11-27

PRIOR PILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

SEQ ID NO 36

LENGTH: 48
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Matches:
Conservative:
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Conservative:
Mismatches:
Indels:
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Indels:
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PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 36, Application US/10023529; Publication No. US20020129388A1; GENERAL INFORMATION:
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; Sequence 36, Application US/10023523
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3.56%
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100.00%
68.75%
3.56%
13
                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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Pred. No.:
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Conservative: Mismatches: Indels:

Length: Matches:

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33 AspGluGluGluGluGluGluGluGluGluAspGluAspGluAsp
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US-10-671-242-36
                           ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-10-275-071-34
                                                   US-10-616-187-36
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Sequence 36, Application No. US20040013668A1

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Ann M.

APPLICANT: Lew, Simon W.

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCIEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616, 289

PRIOR FILING DATE: 2000-0-14

PRIOR PILING DATE: 2000-0-0-0

PRIOR PILING DATE: 1997-11-26

PRIOR PILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1996-11-27

PRIOR FILING DATE: 1996-11-27

PRIOR FILING DATE: 1996-11-27

PRIOR FILING DATE: 1996-11-27

SPRIOR FILING DATE: 1997-11-26

NUMBER OF SEQ ID NOS: 53

LENGTHARE: PREESE (or Windows Version 4.0)

SEQ ID NO 36

LENGTH: 48
                                   GENERAL INCURATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Ann M.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: ATHEROSCLEROSIS

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REPERRING: 10797-004001

CURRENT FILING DATE: 2000-11-2-17

PRIOR APPLICATION NUMBER: US/09/616,289

PRIOR PILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 69/517,849

PRIOR PILING DATE: 1097-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR PILING DATE: 1997-11-27

PRIOR PILING DATE: 1997-10-26

PRIOR PILING DATE: 1997-10-26

PRIOR PILING DATE: 1997-10-26

PRIOR PILING DATE: 1997-10-26

PRIOR PILING DATE: 1997-10-26
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Matches:
Conservative:
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SOFTWARE: FastSEQ for Windows Version 4.0
Publication No. US20020152485A1
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-10-616-187-36
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                    Sequence 34, Application US/10275071; Publication No. US20030186268A1; GENERAL INFORMATION:
APPLICANT: Crouzet, Joel
APPLICANT: Scherman, Daniel
APPLICANT: Wils, Pierre
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100.00%
68.75%
3.56%
18
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1.27e+03
63.00
46.15$
46.15$
      100.00%
80.00%
3.46%
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STRANDEDNESS: double
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Best Local Similarity: 4
Query Match:
DB:
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-329-624-2153
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Pred. No.:
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Sequence 17, Application WS/10275071

Publication No. US20030186268A1

Sequence 17, Application Selected

APPLICANT: Crouzet, Joel

APPLICANT: Scherman, Daniel

APPLICANT: Wils, Pierre

APPLICANT: Blanche, Francis

APPLICANT: Blanche, Francis

TITLE OF INVENTION: PUBLFICATION OF A TRIPLE HELIX FORMATION WITH AN TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE

FILE REFERENCE: 08088.0138-02

CURRENT APPLICATION NUMBER: US/10/275,071

CURRENT APPLICATION NUMBER: 08/580,923

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 1090-05-26

PRIOR FILING DATE: 1099-7-06-09

PRIOR FILING DATE: 1099-7-06-09

PRIOR FILING DATE: 1095-11-08

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PATENTIN VET: 2.1
  APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: 1000-013 0.138-02
CURREMY APPLICATION NUMBER: 09/580,923
PRIOR PILING DATE: 2003-04-07
PRIOR PLILING DATE: 1997-06-09
PRIOR FILING DATE: 1997-06-09
PRIOR FILING DATE: 1997-106-09
PRIOR FILING DATE: 1995-11-08
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 GluAspGluGluGluGluGluGluGluGluGluAspGluAsp 46
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Mismatches:
Indels:
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Matches:
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Matches:
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Pred. No.:
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US-10-275-071-17
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LENGTH: 50
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139 ProProAlaArgProProProProProAlaSerValSerProGlnAlaGluProVal 158
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US-08-781-986A-2153

US-08-781-986A-2153, Application US/08781986A

Publication No. US20030054436A1

GENERAL INFORMATION:
APPLICANT Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34
                                                                                                                                                                     32 GluAspGluGluGluGluGluGluGluGluGluAspGluAsp 46
                                                                                                                                                                                                               ZIP: 208A
ZIP: 208A
ZIP: 208B
ZIP: 208B
COMPUTER READABLE FORM:
MODIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
TILING DATE:
ATTORNEY/AGENT: INFORMATION:
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ON SEQ ID NO: 2153:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
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Conservative:
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RESULT 12
US-10-195-071-14/C
is Sequence 14, Application US/10195071
is Publication No. US2030096271A1
is Publication No. US2030096271A1
is GENERAL INFORMATION:
is APPLICANT: OriGene Technologies
is TILE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
is FILE REFERENCE: 16U 10L C1
is CURRENT APPLICATION NUMBER: US/10/195,071
is CURRENT APPLICATION NUMBER: US 09/930,181
is PRIOR PILING DATE: 2001-08-16
is NUMBER OF SEQ ID NOS: 18
is SOFTWARE: Patentin version 3.1
is SEQ. ID NO 14
is LENGTH: 50
TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas FILE REFERENCE: 160 101 C2
CURRENT APPLICATION UNMER: US/10/195,072
CURRENT FILING DATE: 2002-07-15
FRIOR RPLING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 18
SOOTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 50
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Matches:
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Matches:
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US-10-627-253A-369
; Sequence 369, Application US/10627253A
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                US-10-195-072-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-195-071-14
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DB:
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No.:
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                                                                                                                        Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 ProProAlaArgProProProProProAlaSerValSerProGlnAlaGluProVal 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 175 0 1
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MARK J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-544-776-2 (1-373) x US-10-329-624-2153 (1-50)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 2153
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Scies
STREET: 9410 Key West Avenue
CITY: Rockville
   Sequence 2153, Application US/10329624
Publication No. US20040043037A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2153:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-10-195-072-14/C
is Sequence 14, Application US/10195072
Publication No. US20030092036A1
GENERAL INFORMATION:
APPLICANT: OriGene Technologies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 TrpThrProProAlaPro 164
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                                                          GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.27e+03
63.00
46.15%
46.15%
3.30%
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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DB:
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140 ProAlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrp 159
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDILM TYPE: Diskette
COMPUTER: BEADABLE FORM:
MEDILM TYPE: Diskette
COMPUTER: BEADABLE FORM:
MEDILM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATION DATA:
PRINT APPLICATION UMBER: US (09/962, 055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION NUMBER: US 60/031, 930
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031, 930
FILING DATE: 26-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers LOUIS
REGISTATION NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE: ADDRESSEE: TENETHER TO TENETHER TO TELETHER TO TE
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Matches:
Conservative:
Mismatches:
Matches:
Conservative:
Mismatches:
                                                                                                                                                               US-09-544-776-2 (1-373) x US-10-627-253A-370 (1-50)
                                                                                   Indels:
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LOCATION: 1...45
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.53e+03
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46.43%
46.43%
3.14%
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                      Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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Sequence 370, Application US/10627253A

Publication No. US20040161768A1

GENERAL INFORMATION:
APPLICANT: BRINKMANTION:
TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS

TITLE OF INVENTION: PRESSETANCE-ASSOCIATED PROTEIN (MRP-1) AND THEIR USE IN
TITLE OF INVENTION: PRESSETANCE-ASSOCIATED PROTEIN (MRP-1) AND THEIR USE IN
TITLE OF INVENTION NUMBER: US/10/627,253A

CURRENT APPLICATION NUMBER: PCT/EPO2/00796

PRIOR PILING DATE: 2002-01-25

PRIOR FILING DATE: 2002-01-25

PRIOR FILING DATE: 2001-01-26
                                                                           APPLICANT: HOFFMEYER, SVEN
APPLICANT: HOFFMEYER, SVEN
APPLICANT: HOFFMEYER, SVEN
TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
TITLE OF INVENTION: POLYMORPHISMS IN THERAPEUTIC APPLICATIONS
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
FILE REPERBENCE: VOS-42 CON
CURRENT APPLICATION NUMBER: 2003-07-24
PRIOR APPLICATION NUMBER: PCT/EP02/00796
PRIOR APPLICATION NUMBER: EP 01101651.6
PRIOR PLING DATE: 2003-01-25
PRIOR PLING DATE: 2003-01-26
NUMBER OF SEQ ID NOS: 406
SEQ ID NO 369
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide US-10-627-253A-369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide US-10-627-253A-370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 ProAlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrp 159
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112
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Matches:
Conservative:
Mismatches:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 370
LENGTH: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.37e+03
60.00
46.43%
46.43%
3.14%
     Publication No. US20040161768A1
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                              GENERAL INFORMATION:
APPLICANT: BRINKMANN, ULRICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-544-776-2 (1-373)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-627-253A-370/c
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . No. :
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Indels: Gaps: 3.09**%** 9 Query Match: DB:

00 US-09-544-776-2 (1-373) x US-09-962-055-30 (1-45)

Search completed: August 3, 2005, 23:46:12 Job time : 688 secs

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-MODEL=frame+ pln.model -DEV=xlp
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-Q=/Cgn2 1/USPTO spool p/US09544776/runat_03082005_181346_28256/app_query.fasta_1.519
-DB=Published Applications NA -QFMT=fastap -SUFFIX=pln.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bit s -START=1 -END=-1 -MATRIX=blosum62
-TRANS-bluman40.cdi -LIST=45 -DOCALIGN=200 -THR MXCEN=EDCT -THR MXX=10
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HBAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US09544776 @CGN 1 1 723 @runat_03082005_181346_28256
-NCPU=S -ICPU=3 -NO MMAP -LARGEQUERY /NEG SCORES=0 -WAIT -DSPENDCK=100
-LONGLAG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THERADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEDLDQSPLVSSSDSPPRPQ......VKDAMAKIQAKIPGLKRKAE 373
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	80	ΙD	Description
<b>п</b>	1879	98.4	1122	σ	9 US-09-789-386-5	¥.
0 0	1879	98.4	1610	ο ί	US-09-765-205-5	equence 5, Appli
m <	1879	98.	1610	2 2	US-10-347-669-5	Sequence 5, Appli
יט יי	1879	, 4	2226	7 5	US-IU-956-I5/-453U IIS-10-956-157-4531	Seguence 4530, Ap
9	1879	98.4	2235	14	US-10-060-036-54	Sequence 54, Appl
7	1871	φ.	2052	13	US-10-466-258-3	Sequence 3, Appli
œ	1871	98.0	2052	55	US-10-466-391A-3	Sequence 3, Appli
ο (	•	'n	2782	12	US-10-205-194-165	Sequenc
15	1459.5	٠	3777	nσ	US-U9-789-386-1 IIS-09-893-348-22	Sequence 1, Appil
12	. 4	76.4	3579	, 4	US-10-267-502-212	Semienc
13	• 4		3579	13	US-10-327-213-8	Sequence 8, Appli
14	4	76.4	3579	19	US-10-466-258-8	Sequence 8, Appli
15	40.	76.4	3579	50	US-10-810-653-22	Sequence 22, Appl
16	σ,	76.4	3579	52	US-10-466-391A-8	Sequence 8, Appli
) T	79		4053	nσ	US-US-136-140-3 TIS-09-973-5998-5	Sequence 5, Appli
13	. 4	76.4	4053	13	US-10-717-597-310	Sequence 310. App
20	4	76.4	4623	21	US-10-956-157-4532	Sequence 4532, Ap
21	4	76.4	4632	14	US-10-060-036-53	Sequence 53, Appl
22	1173	٠	4684	0	US-09-893-348-17	Sequence 17, Appl
23	1173	; ⋅	4684	50	US-10-810-653-17	Sequence 17, Appl
24 25	1010	, r	2442	3 5	US-10-26/-502-214	Sequence 214, App
26	•	49.3	3478	21	US-10-956-15/-4528	Sequence 4528, Ap
27	931	8	1400	21	US-10-956-157-9763	Sequence 9763, Ap
28	927	٠	1980	11	US-10-220-891-22	Sequence 22, Appl
53	918	ė,	009	21	US-10-956-157-9764	Sequence 9764, Ap
30	917	٠	799	138	US-10-660-946-2	Sequence 2, Appli
31	917		1500	4.5	US-10-175-523-156	Sequence 156, App
3 6	917	0 00	1785	17	US-10-936-13/-432/ US-10-439-388-62	Sequence 4527, Ap
34	917	8	1785	21	US-10-956-157-1705	Sequence 1705, Ap
35	806	7.	994	1	US-09-978-360A-110	Sequence 110, App
36	904	7.	2610	18	US-10-641-643-382	Sequence 382, App
37	876	•	1798	13	US-10-466-258-10	Sequence 10, Appl
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; sequence ; Patent No	t No. US:	, Application US20020010324	1011 US/ U9/83 0324A1	60	9	
; GENER	GENERAL INFORMATION	MATION:				
, APPL	APPLICANT: MICHALOVICH,	ICHALOV	ICH, DAVID	QIA!		
; APPLI	E OF TWY	I PKINJHA INVENTION:	, KABINDEK KUMA NOVEL COMPOUND	S E	KUMAK	
FILE	FILE REFERENCE	CE: GP-	30165-C	5 5	1	
CURRENT	ENT APPLICATION NUMBER: US/0	APPLICATION NUMBER: US/	NUMBER	33	1/09/789,386	
, CURR	CURRENT FILING DATE	NG DATE	: 2001	-05	0000710	
. PRIOR	R AFFUIC P FILING	DATE.	UMBER: 1999-07		1.0690166	
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| Sequence 5, Application US/09765205
| Patent No. US20020034800A1
| GENERAL INFORMATION:
| APPLICANT: Cao, Li
| TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
| FILE REPERENCE: 1458.004/220130.449
| CURRENT APPLICATION NUMBER: US/09/765,205
| CURRENT FILING DATE: 1201-01-17
| PRIOR PILING DATE: 1998-12-16
| NUMBER OF SEQ ID NOS: 46
| SEQ ID NO 5
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| TYPE: DNN 5
| CURRENT: 1610
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| US-09-765-205-5
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PRIOR FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: DNA
ORGANISM: HOMO SAPIENS
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                                    1610
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                                      Length:
Matches:
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Mismatches:
Indels:
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GENERAL INFORMATION:

ATTLE OF INVENTION:

FILE REFERENCE: 1458.004/200130.449

CURRENT FILING DATE: 1998-12-16

PRIOR FILING DATE: 1998-12-16

NUMBER: 0F SEQ ID NOS: 440

SOFTWARE: PastSEG for Windows Version 3.0

SEQ ID NO 5

SEQ ID NO 5

SEQ ID NO 6

SEQ ID NO 6

SEQ ID NOS: 4

SOFTWARE: PastSEG for Windows Version 3.0

SEQ ID NO 5

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SEQ ID NO 6

SEQ ID NOS: 4

SEQ I
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GCCGGGCTCCCCCTCCTCCCCCGGCCAGGTGAGCCCCCAGGCAGCCCGTGTGGACC
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Db 1032 AAGTTGCGGGGTTTTACCTATGTTGGTGCCTCACA 1091  Qy 321 LeuleulleleunlaturGCGGGTTTTACCTATGTTGGTGCCTCACA 1091  Db 1092 CTACTGAGTGTGGGGTTTTACCTATGTTGGTGCTTTAATGGTTCACA 1091  Qy 321 LeuleulleleunlaturGGTCTTCACTTCAGTGTTTATGGTGGTTTTATGGTGGT 1151  Qy 341 Aladoln1ehapHisTycLeuldyLeulpasctGTTTAAAGTGTTGCTTAA 1211  Qy 361 IleClnalalySileProGlyLeuLyGAATAAGAATGTTAAAGATGCTAAA 1211  Qy 361 IleClnalalySileProGlyLeuLyGAATAAGAATGTTAAAGATGCTAAGCTAAA 1211  Qy 361 IleClnalalySileProGlyLeuLyGAATGAATAAGATGTTAAAGATGCTAAGCTAAA 1211  Qy 361 IleClnalalySileProGlyLeuLyGAAGTGCAAATAAGATGTTAAAGATGTTAAAGATGTTAAAGATGTTAAAGATGTTAAAGATGTTAAAGATGTTAAAGATGTTAAAGATGTTAAAGATGTTAAAGATGTTAAAGATGTTAAAGATGTTAAAGATGTTAAAGATGTTAAAGATGTTAAAAGATGTTAAAAGATGTTAAAAGATGTTAAAAGATGTTAAAAGATGTTAAAAGATGTTAAAAGATGTTAAAAGATGTTAAAAGATGTTAAAAATGTTAAAAGATGTTAAAAATGTTAAAAATGTTAAAAATGTTAAAAATGTTAAAAAA	141 AlakrgProProProProProAlaSerValSerProGlnAlaGluProValIrpThr 160  487 GCCCGGCCTCCCCCCCCCCGGCCGGCGCGGCGCGCGCGC
Alignment Scores:    1.4e-158	321 LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIIleTyrGluArgHisGln 340
Oy 121 SerPheLeuSerAlaAlaAlaValSerProSerLyBLeuProGluAspAspGluProPro 140	Pred. No.: 1.56e-158 Length: 2226 Score: 1879.00 Matches: 370 Percent Similarity: 99.20\$ Conservative: 0 Best Local Similarity: 99.20\$ Mismatches: 3

Qy         341 AlaGinileAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaNetAlaLys           Db         1162 GCACAGATAGATCATTATCTAGGACTTGCAATAAGAATGTTAAAGATGCTATGGCTAAA           Qy         361 IleGlnAlaLysIleProGlyLeuLysAxrGLysAlaGlu           Db         1222 ATCCAAGCAAAATCCTGGATTGAAGGGCAAAGCTGAA           RESULT 6         US-10-060-036-54           Sequence 54, Application US/10060036	; Publication No. US20030073144A1 ; GENERAL INFORMATION: ; APPLICANT: Benson, Darin R. ; APPLICANT: Kalos, Michael D. ; APPLICANT: Persing, David H. ; APPLICANT: Ucdes, Wichael J.	APPLICANT: Jiang, Yuqiu i.  APPLICANT: Jiang, Yuqiu i.  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER  FILE REFERENCE: 210121.56  CURRENT APPLICATION NUMBER: US/10/060,036  CURRENT FILING DATE: 2002-01-30	rΛ	1.56e-158 1879.00 99.20%	99.20% Mismatches: 98.38% Indels: 14 Gaps:	OS-09-544-776-2 (1-973) A US-10-060-038-54 (1-235)  OY	Oy 21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGluGluGluGluGluGluGluGluG	Qy         41 GluGludspGludspGludspLeuGluGluLeuGluValLeuGluArgLysProAla	Qy         61 AlaGlyLeuSerAlaalaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp	81	Qy 101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro	Qy 121 SerPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspAspGluProPro	Qy         141 AlaArgProProProProProProAlaSerValSerProGlnAlaGluProValTrpThr
Query Match:         98.38*         Indels:         0           DB:         21         Gaps:         0           US-09-544-776-2 (1-373) x US-10-956-157-4531 (1-2226)         0         1 MetGluhspLeuhspGlnSerProLeuValSerSerSerAspSerProProArgProGln 20           QY	CCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAAGAAGAGAGGAGGAGGAGG	Algorithms	101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120		ProProAlaProAlaProAlaAlaProProSerThrProAlaAlaProLysArgA 	181 SerSerGlySerValValValAspLeuLeuTyrTrpArgAsplleLysLysThrGlyVal 200	ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerlleValSerVal 	ThrAlaTyr11eAlaLeuAlaLeuLeuSerValThr11eSerbroArg11eTyrLysG1y 	241 ValileGinAlaileGinLysSerAspóluGiyHisProPheArgAlaTyrLeuGluSer 260 	261 GluvalalaileSerGluGluLeuvalGlnLysTyrSerasnSeralaLeuGlyHisVal 280 		LysphealaValleuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 	321 LeuLeulleLeuAlaLeulleSerLeuPheSerValProValIleTyrGluArgHisGln 340 

	Cy 321 LeuLeulleLeualaLeutleSerLeuPheSerValProVallIeTyrGluargHisGln 340 1027 CTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTATTATGAACGGCATCAG 1086 Cy 341 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 360
1 ProprohlaprohlaprohlaplaproproserThrprohlaplaceCccccccccccccccccccccccccccccccccccc	Pred. No.: 7.31e-158 Length: 2052 Score: 1871.00 Matches: 368 Percent Similarity: 98.93\$ Conservative: 1 Best Local Similarity: 98.66\$ Mismatches: 4 Query Match: 19.796\$ Indels: 0 DB:

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                        ThralaTyr11ealaLeuAlaLeuLeuSerValThr11eSerProArg11eTyrLysG1y
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; Publication No. US20030134301A1
; GENERAL INFORMATION:
    APPLICANT: Warner-Lambert Company
    APPLICANT: Dixon, Alistair
    APPLICANT: Brooksbank, Robert
    APPLICANT: Pinnock, Robert
    APPLICANT: Pinnock, Robert
    TITLE OF INVENTION: Identification and Use of
    FILE REFERENCE: WL-018201
    CURRENT APPLICATION UNMBER: US/10/205,194
    CURRENT FILING DATE: 5200-07-24
    FRIOR FILING DATE: 2001-07-27
    NUMBER OF SEQ ID NOS: 177
    SOFTWARE: PATCHING UNCE: 2.1
    SEQ ID NO 165
    LENGTH 12782
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US-10-205-194-165
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                                                                                                                                                                          Sequence 3, Application US/10466391A
Publication No. US20040146953A1
GENERAL INPORMATION:
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: ASSAY
CURRENT APPLICATION WHOBER: US/10/466,391A
CURRENT FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 2052
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ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (67)..(1188)
US-10-466-391A-3
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US-10-466-391A-3
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                                                                                                                 GRUEGEL OF APPLICATION US/09789386
FRACEL NO. US20020010324A1
GRNERAL INFORMATION:
APPLICANT: MICHALOVICH, DAVID
APPLICANT: MICHALOVICH, DAVID
APPLICANT: PRINJHA, RABINDER KUMAR
TITLE REPERBNCE: GP-30165-C1
CURRENT FILING DAYE: 2001-02-21
FRIOR APPLICATION NUMBER: U.K. 9916898.1
FRIOR FILING DATE: 1999-07-19
FRIOR FILING DATE: 1999-07-22
FRIOR FILING DATE: 1999-07-22
FRIOR FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FRSESE FESTERE OF SEQ ID NOS: 6
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                              1.38e-120
1459.50
31.04%
31.04%
76.41%
                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: HOMO SAPIENS
US-09-789-386-1
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-09-789-386-1
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                                          20 GlnProAlaPheLysTyrGlnPheValArgGluProGluAspGluGlu---GluGluGlu
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                            MetGluAspLeuAspGlnSerProLeuValSerSerSer-
        US-09-544-776-2 (1-373) x US-10-205-194-165 (1-2782)
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APPLICANT: BESERVAN, falson APPLICANT: BESERVAN, falson APPLICANT: MOSONEGO, Alon APPLICANT: MOSONEGO, Alon APPLICANT: MOSONEGO, Alon APPLICANT: MOSONEGO, Alon TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES; FILE REFERENCE: ELS-SCHWARTZ-22; CURRENT APPLICATION NUMBER: US 09/314,161 PRIOR FILING DATE: 1999-05-19 PRIOR FILING DATE: 1999-05-19 PRIOR FILING DATE: 1999-05-19; PRIOR FILING DATE: 1998-0-21 PRIOR FILING DATE: 1998-0-21 PRIOR FILING DATE: 1998-0-19; SOFTWARE: PARCHING DATE: 1998-0-19; NUMBER OF SEQ ID NOS: 29; SOFTWARE: PARCHIN VERSION 3.1
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2581 GATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATCAGTTCTAAAACTGAT 2640
                                                                      2641 TCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCCACAAAAGTGAAATT 2700
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

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                                                                                                                                                              ATGGAAGACCTGGACCAGTCTCCTCTGGTCTCCTCGGACAGCCCCACCCCGGCCGCAG
                                                                                                                                                                                          ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGluGluGluGlu
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                                                     Length:
Matches:
Conservative:
Mismatches:
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                                                                                               Indels:
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1459.50
31.04%
31.04%
76.41%
; LOCATION: (1)..(3579)
; OTHER INFORMATION:
US-09-893-348-22
                                                                                     Best Local Similarity:
                                                                          Percent Similarity:
                                           Alignment Scores:
Pred. No.:
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Sequence 22, Application US/09893348
Patent No. US20020072493A1
GENERAL INFORMATION:
APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, Irun R.

us-09-544-776-2.p2n.rnpb

8 8	181 SerSerGlySerVal	Db 1621 G	GAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAGGAAGCATGTGAA 1680
} &		Qy 185 -	185
<b>3</b> 8		Db 1681 A	AGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAAATGGACTTGGTT 1740
ځ		Qy 185 -	185
S 8	1 CAAGAGGATTTCCCATCTGTGCTTGAAACTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTC	Db 1741 C	CAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTTTGCCCATCATTT 1800
\$		Qy 185 -	185
S &	しょうけん かいかい かんかん かんかん かんかん かんかん かんかん かんかん かん	Db 1801 G	GAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATGGAAGCACCATTG 1860
3 8	777447 1647 7647 774 7464 777 777 777 777 777 77	Qy 185 -	185
5 8	) T ACTIGARAGARACACTTICARARARARAGGTTARARAGAGGTTCTTARARAGAGGTCT	Db 1861 A	AATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCATCACCATTAGAA 1920
ò		185	
g q	1 AAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATACTCAGAAATG	Db 1921 G	GCTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAACCCCCCCC
8		Qy 185 -	185
. A	1 GGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCAAATCCTAGG	1981	GAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAAGAAATTAAAGAGCCT 2040
غ ا		Qy 185 -	185
S 8	3 GAAGAAATAATCGTGAAAAATAAAGATGAAGAAAGGTTAGTTA	Db 2041 G	GAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATTGCATGTGAT 2100
}		Qy 185 -	185
3	ション・コード・コード・コード・コード・コード・コード・コード・コード・コード・コード	Db 2101 T	TIAATITAAAGAAACAAAGCITTCTGCTGAACCAGCTCCGGATTTCTCTGATATTCAGAA 2160
g 8	CALMAI CANCARGAGI IACCIACAGCI CI IACIMAA I IGGI IMAAGAGGA I GAMGI IGIG	Qy 185 -	185
Š 18	CHE WILL CHE A CALL A C	Db 2161 A	ATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTTGAAGATTCCTCACCT 2220
9 (	ICITCAGARAMAGCAAAAGATIIIAA IGAARAGAGIIGCAGIGGAAGCICCIAIG	Oy 185 -	185
ਨੇ 1	**************************************	Db 2221 G	GATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCACAAAAACAA 2280
g (	AGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTGAAAGATAGTAGTAAG	Qy 185 -	185
S	183	Db 2281 G	GATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTTGAGTCAATGATA 2340
g ·	GAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAAGCAACTTGGAAAAGTAAAGTG	Qy 185 -	185
<i>&amp;</i> ∶		Db 2341 G	GAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGAGG
Ω Ω	GATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAAGATAGTGAGAGT	Qy 185 -	185
<b>ह</b> ें :		Db 2401 G	GAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCTGATGAAGTTTCA 2460
qq	i agiaaigaigatactiviticcccagiacgccagaaggiaiaaaggaicgiccaggagca	Qy 185 -	185
<b>&amp;</b> :		2461	ACAITGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTCAGTACTGCAGTTTAT 2520
g G	1 TATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGGGATTGCAACAACATTTTT	Qy 185 -	185
È	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Db 2521 T	TCAAATGATGACTTATTTTTTTTTTTAAGGAAGCACAGATAAGAGAAACTGAAACGTTTTCA 2580
q	CCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA	Oy 185 -	185
à		2581	GATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATCAGTTCTAAAACTGAT 2640
<b>Q</b>	AAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAACCTTTTCTTGTA	Qy 185 -	185
ò		2641	TCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCCACAAAAGTGAAATT 2700
අු	GCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACAAAGGTGACTGAG	Oy 185 -	185
ò	185 185		

; TYPE: DNA ; ORGANISM: Homo sapiens US-10-267-502-212	1.38e-120 Length:	Conservative: 0 Mismatches: 3	76.41% indels: 18 Gaps:	US-09-544-776-2 (1-373) x US-10-267-502-212 (1-3579)	Qy 1 MetGluAspLeuAspGlnSerProLeuValSerSerAspSerProProArgProGln 20	Db 1 ATGGAAGACCTGGACCTCTCTCTTCGTCCTCGGACAGCCCCGGCGCAG 60	21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGluGluGluGluGluGluGluGluG	61	Qy 41 GluGluAspGluAspGluAspLeuGluGluCeuGluValLeuGluArgLysProAla 60	Qy         61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80           Db         181 GCCGGGCTCTCCGCGGCCCCAGTGCCCACCCCCTGCCGCGCGCG	81 PheGlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal	DD 241 TICGGAAATGACITCGTGCCGCCGGCGCCCCGGGGGGCCCCGGCCGCCGTCCCCCC	301 GCCCGGGAGCGGCAGCCTTTGGAACCCGAGCCCGGTGTCGTCGTCGTCGTCGTCGCCCGCC	Qy 121 SerPheLeuSerAlaAlaAlaAlaFroSerIysLeuProGluAspAspGluProPro 140	Qy         141 AlaArgProProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160			Db 541 TCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCTGTGATA 600	Qy 185 185	Db 601 CGCTCCTCTGCAGAAATATGGACTTGAAGGAGCAGCCAGGTAACACTATTTCGGCTGGT 660	Qy 185 185	Db 661 CAAGAGGATTICCCAICTGTCCTGCTTGAAACTGCTGCTTCTTTCTTCTTCTTCTTCTTCTT 720	Qy 185 185	Db 721 CTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACAGTATTACCC 780	Qy 185 185	Db 781 ACTGAAGGAACACTTCAAGAAATGTCAGTGAAGCTTCTAAAGAGGTCTCAGAGAAGGCA 840	Qy 185 185	Db 841 AAAACTCTACTATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATACTCAGAAATG 900
Db 2701 GCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACAGAATTGCCCCATGACTTTCT 2760 Qy 185 185	Db 2761 TTGAAGAACATACAACCCAAAGTTGAAGAAAATCAGTTTCTCAGATGACTTTTCTAAA 2820	2821 AATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCTGCTTTGGCCACT 28	Qy 185 185	Db 2881 CAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAAGAAGAGGAGAAAAAA 2940	Qy 185 185	Db 2941 CTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTCAGCAGAGCTG 3000	186ValValAspLeuLeuTrpArgAspIleLysLysThrGlyValVal	Db 3001 AGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTG 3060	Oy 202 PheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThr 221	Qy       222 AlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGlyVal 241         Db       3121 GCCTACATTGCCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTG 3180	242 IleGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGlu	DD 3181 AICCAAGCIAICCAGAAAICAGAIGAAGCCACCCAITCAGGGGAIAICIGGAAICIGAA 3240 Ov 262 ValAlaileSerGluGluLeuValGlmivsTvrSerAsmSerAlaLeuGlvHisValAsm 281	3241 GTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAC	Qy 282 CysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLys 301 	Qy 302 PheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeu 321 	LeulleLeuAlaLeulleSerLeuPheSerValProVallleTyrGluArgHisGlnAla	342 GlnileAepHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIle	Db 3481 CAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTAAGGCTAAAATC 3540	Qy 362 GlnAlaLysIleProGlyLeuLysArgLysAlaGlu 373	Db 3541 CAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAA 3576	RESULT 12 11S-10-267-502-212	; Sequence 22, 12, Application US/10267502	GENERAL NO. USZUCŁOWILIONAL GENERAL PRORMATION NADITIONAL KIR. ZAROJOK	; AFPLICANT: Galant, Dance ; AFPLICANT: Galant, Inked Genee ; THIR OF INVENTION: Obesity Linked Genee	FILE REFERENCE: LSD-07416 FILE REFERENCE: LSD-07416 FILEDER PROPERTY ADDITIONAL NUMBER 115/10/267 6	CORRENT AFFILENTION NOTION: 05/10/20/20/20/20/20/20/20/20/20/20/20/20/20	; SOFTWARE: Patentin version 3.2 sro ID NO 212	; SEQ ID NO 212 ; LENGTH: 3579

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કે	185	qQ	1981 GAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAAGAAATTAAAGAGCCT 2040
q	901 GGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCAAATCCTAGG 960		
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qq	961 GAAGAAATAATCGTGAAAATAAAGATGAAGAAGAAGTTAGTT		GAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATTCTATTGCATGTGAT
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q	1021 CATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGATGAAGTTGTG 1080	qa	2101 TTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTCTCTGTGATTATTCAGAA 2160
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: A	TCTTCAGAAAAAGGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTGGAAGCTCCTATG	q	2161 ATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTTGAAGATTCCTCACCT 2220
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q	1141 AGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAAGATAGTAAG 1200	٠	GATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCACAAAAAAA
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qq	1201 GAAGATAGTGATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTGGAAAGTAAAGTG 1260		GATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTTGAGTCAATGATA
ò	185 185		
q	1261 GATAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAAGATAGTGAGAGT 1320		Gaatatgaaaataaggaaaaactcagtgctttgccacctgagggagg
ò	185 185		
g	1321 AGTAATGATGATGATTCTTTCCCCAGTACGCCAGAAGGTATAAAGGATCGTCCAGGAGCA 1380	q	2401 GAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCTGATGAAGTTTCA 2460
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3 E	TATATCACATGTGCTCCCTTTAACCAGCAACTGAGGAATTGAGAACAAATGAAACAAAC	qa	2461 ACATTGAGGAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTCAGTACTGCAGTTTAT 2520
3 8	***************************************	ò	185 185
à ·		qq	2521 TCAAATGATGACTTATTTTATTTCTAAGGAAGCACAGATAAGAGAAACTGAAACGTTTTCA 2580
qa ,	cctttgttaggagatcctacttcagaaaataagaccgatgaaaaaaaa	ò	185 185
ò	185	q	2581 GATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATCAGTTCTAAAACTGAT 2640
g	1501 AAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAACCCTTTTCTTGTA 1560	è	5861
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q	1621 GAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAGGAAGCATGTGAA 1680		GCIAAIGCCCCGGAIGGAGGIGGICAIIGCCIIGCACAGAAIIGCCCCCAIGACCIIICI
ò	185 185		***************************************
qq	1681 AGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAAATGGACTTGGTT 1740		TIGAAGAACATACAAACCCAAAGTIGAAGAGAAAATCAGTIICICAGATGACTIITICTAAA
ò	185 185		
q	1741 CAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTTTGCCCCATCATTT 1800		AATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCTGCTTTGGCCACT
È	185 185		
qa	1801 GAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATGGAAGCACCATTG 1860		Caagcagagatagagagcatagttaaacccaaagttcttgtgaaagaaggtgagaaaaa
ò	185 185		
qq	1861 AATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCATCACCATTAGAA 1920		CTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTCAGCAGAGGCTG
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සු	1921 GCTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAACCCCCCCC	8 8	3001 AGIAAAACITCAGITGITGACCICCTGIACIGGAGAGACAITAAGAAGACTGGAGIGGIG 3060 303 bhacilallacarfanbhaianfan an an CarfanGarfanmhrus Ibhacarflavalcarvalmhr 221
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GluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla	301 GCCCCGGAGCGGCCCCTTTGGGACCCGGGGTCGTCGTCGACCGTGCCCGCGCCCA 360 121 SerPheLeuSerAlaAlaAlaAlaValSerProSerLysLeuProGluAspAspGluProPro 140	421 GCCCGGCCTCCCCCCCCCGGCCAGCGTGAGCCCCCAGGCAGCCCGTGTGGACC 480 161 ProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArgG1y 180 161 ProProAlaProAlaProAlaProProSerThrProAlaAlaProLysArgG1y 180 181 CCGCCAGCCCCGGCCCCCCCCCCCCCCCCCCCCCCCCC		601 CGCTCCTCTGCAGAAATATGGACTTGAAGGAGCAGCCAGGTAACACTATTTCGGCTGGT 660	661 CAAGAGATTTCCCCATCTGTTGAAACTGCTGCTTCTTTCT	CTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACAGTATTACCC 78	actgaaggaacacttcaagaaaatgtcagtgaagcttctaaagaggtctcagagaaggca	185	185 185 185 185 185		gaagaaataatcgtgaaaaataaagatgaagaagagagag	185 185 185 185 185 185		TCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTGGAAGCTCCTATG	185
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222 AlaTyrileAlaLeuAlaLeuLeuServalThrileSerProArgileTyrLygGCGTAACA 222 AlaTyrileAlaLeuAlaLeuLeuServalThrileSerProArgileTyrLygGlyval 3121 GCTACTTGGCCTGGCCTGTGGCTTGTGGGATTACAGGGTTGTGAGGCGTAG  242 IleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGlu 3181 ATCCAAGCTTCCGGGATTGGTAGGTTGGGTTGGATTGGA	Oy 282 CysThrileLysGluLeuArgArgLeuPheLeuValAppAspLeuValAspSerLeuLys 301	Qy         322 LeulleLeuAlaLeulleSerLeuPheSerValProValIIETyrGluArgHisGlnAla 341           Db         3421 CTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT	Oy 362 GInalaLysIleProGlyLeuLysArgLysAlaGlu 373 	RESULT 13 US-10-327-213-8 ; Sequence 8, Application US/10327213	; Publication No. US20040121341A1 ; GENERAL INFORMATION: ; APPLICANT: FILBIN, MARIE T. : APPLICANT: DOMRHICONI. MARCO	HEREICANT: CAO, ZIXUAN  TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)  TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION  TITLE DEPENDENCE. CHAN ACAD.	FION NUMBORES 20 NOS: 43	; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 8 ; LENGTH: 3579 . TYDE: DAA	; ORGANISM: Homo sapiens US-10-327-213-8	ent Scores: 1.38e-120 Length: 1.38e-120 No.:	larity: 31.04% imilarity: 31.04%	Indels: Gaps:	-09-544-776-2 (1-373) x US-10-327-213-8 (1-3579)	Oy         1 MetGludspleudspGludSerFoleuValSerSerSerSepSerFolerOatgerodin 20           1	Oy 21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGluGluGluGluGluGluGluGluG

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GATAAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAAGGATAGTGAGAGT	2341 GAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGAAGGAA
185	Qy 185 185
AGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAAGGATCGTCCAGGAGCA	2401 GAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCTGATGAAGTTTCA
185 185	185
1381 TATATCACATGTGCTCCCTTTAACCCCAGCAACTGAGAGCATTGCAACAAACA	2461 ACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTCAGTACTGCAGTTTAT
185 185	185
1441 CCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA	2521 TCAAATGACTTATTTATTTCTAAGGAAGCACAGATAAGAAAACTGAAACGTTTTCA
185 185	185
1501 AAGGCCCAAATAGTAACAGAAGAATACTAGCACCAAAACATCAAACCTTTTCTTGTA 1560	UD 2581 GAIICHAICICCAAIIGAAAIIAIAGAAIIGAGIICCCIACAIIGAICAGIICCAAAIIGAAIIAGAAIAGAAIAGAAIAGAAAIIAGAAIAGAAAIAGAAAIAGAAAIAGAAAAIAGAAAAIAGAAAAAIAGAAAAAA
	2641 TCATTITCTAAATTAGCCAGGAATATACTGACCTAGAAGTATCCCAACAAAAGTGAAATT
1561 GCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACAAAGGTGACTGAG 1620	Oy 185 185
	Db 2701 GCTAATGCCCCGGATGGAGCTGGTCATTGCCTTGCACAGAATTGCCCCATGACCTTTCT 2760
GAAGICGIGGCAAACAIGCCIGAAGGCCIGACICCAGAIITAGIACAGGAAGCAIGIGAA	Qy 185 185
185	Db 2761 TTGAAGAACATACAACCCAAAGTTGAAGAAAATCAGTTTCTCAGATGACTTTTCTAAA 2820
	Qy 185 185
135	Db 2821 AATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCTGCTTTGGCCACT 2880
	Qy 185 185
GAAGAGTCAGAAGCTACTTCACCAGTTTTGCCTGACATTGTTATGGAAGCACCATTG	2881 CAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAAGGAGCTGAGAAAAA
185 185	1982
1861 AATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCATCACCATTAGAA 1920	Db 2941 CITCCITCCGAIACAGAAAAGAGGACAGAICACCAICIGCIAIAITITCAGCAGAGCIG 3000
185 185	1001 acasasacumoracumoracumoracumoracacacacacacacacacacacacacacacacacacac
1921 GCTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAACCCCCCCC	202 PheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThr
	3061 TTTGGTGCCAGCCTATTCCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACA
1981 GAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAAGAATTAAAGGCCT 2040	Ov 222 AlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGlyVal 241
185	3121 GCCTACATTGCCTTGGCCCTGCTGTACATCATTAGGATATACAAGGGTGTG
	242 IleGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGlu
TTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTCTCTGATTATTCAGAA	Db 3181 ATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCTATCTGGGAATCTGAA 3240  Qy 262 ValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsn 281
185	Db 3241 GTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAC 3300 Ov 282 CvsThrIleivsGluleuArdArdLeuPalAspaeleuValAspaeluValAspSerLeuLvs 301
185 185 2221 GATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCACAAAACAA 2280	3301 TGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTTGAAG
185 185	Oy 302 PheAlaValleuMeTTrpValPhrTyTyValGlyAlaLouPheAsnGlyLeUinTrleU 321

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Qy       141 AlaArgProProProProProAlaSerValSerProGlnAlaGluProValTrpThr         b       421 GCCCGGCCTCCCCCCCCCCGGCCAGGCGCAGGCCCTGTGGACC         Qy       161 ProProAlaProAlaAlaProAlaAlaProProSerThrProAlaAlaProLysArgGly         Db       481 CCGCCAGCCCGCTCCCGGCCCCCCTCCACCCGCCGCCCCCAGCGCGCGC	Db 601 CGCTCCTCTGCAGAAATATGGACTTGAAGGAGCAGCCAGGTAACACTATTTCGGCTGGT  Qy 185	185 961 185 1021 185 1081	Db 1141 AGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGCGAAAGTAAGT
3361 TTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTA 3420 322 LeulleLeualaLeulleSerLeupheSerValProVallleTyrGluArgHisGlnAla 341 [	RESULT 14 US-10-466-258-8 Sequence 8, Application US/10466258 Sequence No. US20040132096A1 SEQUENCE WOOD TO	res: 1.38e-120 Length: 3579 arity: 31.04* Matches: 370 milarity: 31.04* Mismatches: 3 76.41* Indels: 2 (1-373) x US-10-466-258-8 (1-3579) MetGluAspLeuAspGlnSerProLeuValSerSerSerRspSerProProArgProGln	1

2700 3000 3180 2760 2820 2880 3060 3120 3300 3360 3420 3480 3540 1581 GATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATCAGTTCTAAAACTGAT 2640 2881 CAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAGAAGCTGAGAAAAA 2940 3181 ATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAA 3240 281 241 321 341 201 221 261 301 361 TTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTAATGGTCTGACACTA TCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCCACAAAAGTGAAATT 701 GCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACAGAATTGCCCCATGACCTTTCT 2761 TTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGATGACTTTTCTAAA 2821 AATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCTGCTTTGGCCACT CTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTCAGCAGAGCTG PheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThr 3121 GCCTACATTGCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTG IleGlnAlaileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGlu ValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsn GTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAC CysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLys PheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeu LeulleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAla GlnileAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysile 3481 CAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATC AlaTyrileAlaLeuAlaLeuLeuSerValThrIleSerProArgileTyrLysGlyVal 3541 caagcaaaarcccrggarrgaagcgcaaagcrgaa 3576 GlnAlaLysileProGlyLeuLysArgLysAlaGlu 373 2641 2941 202 242 3241 3301 302 3361 342

<sup>;</sup> Sequence 22, Application US/10810653; Publication No. US20040253218A1; GENERAL INFORMATION: BISENBACH-SCHWARTZ, Michal APPLICANT: COHEN, Irun R.

	QQ	481 CCGCCAGCCCCCGCCCCCCCCCCCCCCCCCGGCCGCCCAAGCGCAGGGGC 540
MOSONEGO, Alon MOALEM, Gila	ò	181 SerSerGlySerVal 185
NVENTION: ACTIVATE ENCE: EIS-SCHWARTZ	q	
AFFLICATION NUMBER: US/10/810,653 FFILING DATE: 2004-03-29	ò	185 185
6-25	đ	601 CGCTCCTCTGCAGAAATATGGACTTGAAGGAGCAGCCAGGTAACACTATTTCGGCTGGT 660
	ò	185 185
APPLICATION NUMBER: US 09/218,2// 15.10.00 DATE: 1998-12-22	q	661 CAAGAGGATTTCCCAFCTGTCCTGCTTGAAACTGCTGCTTCTTTCTTCTTCTTGTCTCCT 720
	ò	185 185
386 388	qq	721 CTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACAGTATTACCC 780
NUMBER OF SEQ ID NOS: 29 SOFTWARE: PatentIn version 3.1	ò	185 185
SEQ ID NO 22 LENGTH: 3579	qg	781 ACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCAGAGAGGCA 840
TYPE: DNA ORGANISM: Homo sapiens	ò	185 185
CDS	Ор	841 AAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATACTCAGAAATG 900
j DOTER INCRMATION:	ò	185 185
77-500	qq	901 GGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCAAATCCTAGG 960
0	È	185 185
1459.50 Matches: 31.04% Conservative:	Ор	961 GAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAAGTTAGTT
: 51.04 Mismacches: 76.41% Indels:	ò	185 185
20 Gaps	đ	1021 CATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGATGAAGTTGTG 1080
-Z (I-3/3) X US-IU-8IU-653-ZZ (I-35/9)	λõ	185 185
I METGLIMABLEHMANDGILDSELFTOLENVALDSELFGENSELFRONDERFYTORTOGILD ZU	qq	1081 TCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTGGAAGCTCCTATG 1140
######################################	ò	185 185
FIGHT	đ	1141 AGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAAGATAGTAAG 1200
\(\text{Coct} 1.6.12.12.13.16.16.16.16.16.16.16.16.16.16.16.16.16.	ò	185 185
4. detectorative de la company	ф	1201 GAAGATAGTGGATAGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTGGAAAGTAAAGTG 1260
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	qа	1261 GATAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAAGATAGTGAGAGT 1320
Dhec] vaenaenoheVal Drobrok   a brokrd?   voheTenDrok   a bla brobroVal	ò	185 185
	ф	1321 AGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGATCGTCCAGGAGCA 1380
	ò	185 185
101 Atariogiumiggiiricostiiphabproseiricostiiriseariohaario 120	ą	1381 TATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCAACAACATTTT 1440
GCCCCGGGGCGGCGCCGTCTTGGGGGCCCGGGTGGTCGGCCGGTGCCCGGCCGCC	ò	185 185
121 SETPINLEUSSTATAALAATAVAISSETETSSETLYSLEURISTOGIUASDAADGIUUTORIO 140 	đ	1441 CCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA
1 a a reproproproproproa a serva Serval arbrog in a laging trumbr	ò	185 185
GCCCGGCCTCCCCCCCCCCCGGCCAGCGTGAGCCCCCCAGGCAGAGCCCGTGTGGACC	qo ,	AAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAACCTTTTCTTGTA
161 ProProAlaProAlaProAlaAlaProProSerThrProAlaAlaProJysArgArgGly	දු දු	185

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August 3, 2005, 17:11:04; Search time 1407 Seconds (without alignments) 10304.249 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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20: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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24: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
25: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
26: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-544-776-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0 Maximum DB seq length: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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                                                                                                                                                                                                                                                                   Run on:
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			Description	Sequence 743, App	Sequence 34, Appl	Sequence 17, Appl	Sequence 36, Appl	Sequence 36, Appl	Sequence 36, Appl	Sequence 36, Appl
SUMMARIES			ID	50 17 US-10-131-827-743	US-10-275-071-34	US-10-275-071-17	US-09-962-055-36	US-09-976-740-36	US-10-023-529-36	US-10-023-523-36
			DB	17	16	16	0	σ	13	13
		Query	Length	50	48	20	48	48	48	48
	ф	Query	Match	2.2	1.7	1.7	1.6	1.6	1.6	1.6
			Score	50	37.4	37.4	35.2	35.2	35.2	35.2
		Result	No.		8	m	4	S	9	7

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Gaps

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Indels

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Length 50;

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BLINDING PROTEINS AND THEIR USES IN DIAGNOSING AND TREATING ATHEROSCLEROSIS
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TELECOMMUNICATION INFORMATION:
TELEPHON: 617/542-5070
TELEFPX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 GACGAGGAGGAAGAAGAGGAGGAGGAAGAGGAGGACGAGGACGAAGAC 281
                                                                                                                                                                                                           Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-10-275-071-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                              Score 37.4; DB 16;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35.2; I
Pred. No. 82;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSER: 1918 & Richardson P.C.
STRRET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Coding Sequence
LOCATION: 1...48
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                    Sequence 36, Application US/09962055
Patent No. US20020052033A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lees, Ann M.
Lees, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch
1.6%;
1. Similarity 83.3%;
40; Conservative (
                                                                                                              Query Match
Best Local Similarity 87.2%;
Matches 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Law, Simon W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ropology: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 40; Conservi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                         RESULT 4
US-09-962-055-36
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APPLICANT: Scherman, Daniel
APPLICANT: Scherman, Daniel
APPLICANT: Wils, Pierre
APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: INMOBILIZED OLIGONUCLEOTIDE
FILE REFERENCE: 0888.0138-02
CURRENT FILING DATE: 2003-04-07
PRIOR PLICATION NUMBER: 09/580,923
PRIOR FILING DATE: 1997-06-09
PRIOR PLILIG DATE: 1997-06-09
PRIOR PLILIG DATE: 1997-06-09
PRIOR PLILING DATE: 1995-11-08
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver: 2.1
LENGTH: 50
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                                                                                                                                                                                                                                                                                          APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORWATION WITH AN TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
FILE REPERENCE: 08888.0138-02
CURRENT APPLICATION NUMBER: US/10/275,071
CURRENT PILING DATE: 2003-04-07
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 1997-06-09
PRIOR FILING DATE: 1997-06-09
PRIOR FILING DATE: 1997-06-09
PRIOR FILING DATE: 1995-11-08
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                          TGTGGTTTAAGCTGTAAATCTGTGGAATGCATTGAACTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.7%; Score 37.4; I
Best Local Similarity 87.2%; Pred. No. 22;
Matches 41; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/10275071
Publication No. US20030186268A1
GENERAL INFORMATION:
APPLICANT: Crouzet, Joel
APPLICANT: Scherman, Daniel
                                                                                                                                                         Sequence 34, Application US/10275071
Publication No. US20030186268A1
GENERAL INFORMATION:
APPLICANT: Crouzet, Joel
APPLICANT: Scherman, Daniel
APPLICANT: Wils, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 34
LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-275-071-17
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Gaps

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Indels

Length 48;

48

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Gaps

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Sequence 36, Application US/10023523

Sequence 36, Application US/10023523

Publication No. US20020152485A1

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lew, Simon W.

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE OF INVENTION: ATHEROSCLEROSIS

FILE REPERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616,289

PRIOR PILING DATE: 2001-12-17

PRIOR PILING DATE: 2000-03-02

PRIOR FILING DATE: 2000-03-02

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-27

PRIOR FILING DATE: 1997-11-26

PRIOR PRIOR FILING DATE: 1997-11-26

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Publication No. US20040013668A1

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REPERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/10/616,187

CURRENT PILING DATE: 2003-07-09

PRIOR FILING DATE: 2000-03-07

PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 09/517,849
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                                                                                                                                                                                                                                                                                      Length 48;
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                                                                                                                                             Indels
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                                                                  Score 35.2; DB 13;
Pred. No. 82;
0; Mismatches 8;
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Best Local Similarity 83.3%; Pred. No. 82;
Matches 40; Conservative 0; Mismatches 8;
                                                                  Query Match 1.6%;
Best Local Similarity 83.3%;
Matches 40; Conservative (
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US-10-023-529-36
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                                                                                                                                                                                                                                   GENERAL INVENTALION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REPERRECE: 10797-004001
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/976,740
PRIOR APPLICATION NUMBER: US 60/011,930
PRIOR APPLICATION NUMBER: US 60/011,930
PRIOR PELING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1997-106-03
NUMBER OF SEQ ID NOS: S3
SOFTWARE: FASTERQ for Mindows Version 4.0
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APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCIEROSIS
FRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-27
PRIOR PILING DATE: 1997-11-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 35.2; DE; Pred. No. 82; 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 48
                                                                                                                                         Sequence 36, Application US/09976740; Publication No. US20020194633A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36, Application US/10023529; Publication No. US20020129388A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.6%;
Best Local Similarity 83.3%;
Matches 40; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                  RESULT 5
US-09-976-740-36
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1,4-DIHYDRO-4-OXO-1,8-NAPTHTHYRIDINE ANALOGS
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1.3%; Score 29.6; DB 21; Length 46;
Best Local Similarity 79.5%; Pred. No. 2.2e+03;
Matches 35; Conservative 0; Mismatches 9; Indels
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; Gequence 9, Application US/10903975
; Publication No. US20050085468A1
GENERAL INFORMATION:
; APPLICANT: WHITTEN: Jeffrey P.
; APPLICANT: SIDDIGUI-JAIN, Adam
; APPLICANT: MORAN, Terrance
; TITLE OF INVENTION: SUBSTITUTED QUINOBENZOXOZINE ANALOGS
; FILE REFERENCE: 5322300120
; CURRENT APPLICATION NUMBER: US/10/903,975
CURRENT FILING DATE: 2004-07-30
; PRIOR PELICATION NUMBER: US 60/461,21
; PRIOR PELICATION NUMBER: US 60/461,21
; PRIOR PELICATION NUMBER: US 60/463,171
; PRIOR PELICATION NUMBER: US 60/519,535
; PRIOR PELICATION NUMBER: US 60/532,727
; PRIOR PELICATION NUMBER: US 60/532,727
; PRIOR FILING DATE: 2003-10-12
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 20
; SEQ ID NOS: 46
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Publication No. US20030228302A1
GENERAL INFORMATION:
APPLICANT: Crea, Roberto
TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
FILE REFERENCE: 1551.2001-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 GAGGACGAGGAGGAGAAGAGGAGGAGGAAGAGGAGGACGAGGA 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                   FILE REPERENCE: 5322320001200
CURRENT APPLICATION NUMBER: US/10/820,487
CURRENT FILING DATE: 2004-04-07
PRIOR PILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-11-12
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SCOFTWARE: 46
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Matches 35; Conserv
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US-10-903-975-9
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| Sequence 36, Application US/10671242
| Publication No. US20040040049A1
| GENERAL INFORMATION:
| APPLICANT: Lees, Ann M. |
| APPLICANT: Lees, Robert S. |
| APPLICANT: Lees, Robert S. |
| APPLICANT: Lees, Robert S. |
| APPLICANT: Lees, Ann M. |
| TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: ATHEROSCLEROSIS |
| FILE REFERENCE: 10797-004001 |
| CURRENT APPLICATION NUMBER: US/09/616,289 |
| PRIOR PLILING DATE: 2000-07-14 |
| PRIOR PLILING DATE: 2000-07-14 |
| PRIOR PLILING DATE: 2000-03-02 |
| PRIOR PLILING DATE: 1997-11-26 |
| PRIOR APPLICATION NUMBER: US 69/031,930 |
| PRIOR PLILING DATE: 1997-11-27 |
| PRIOR PLILING DATE: 
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1.6%; Score 35.2; D
Best Local Similarity 83.3%; Pred. No. 82;
Matches 40; Conservative 0; Mismatches
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1.6%; Score 35.2; D
Best Local Similarity 83.3%; Pred. No. 82;
Matches 40; Conservative 0; Mismatches
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APPLICANT: SCHWAEBE, Michael
APPLICANT: MORAN, Texrance
TITLE OF INVENTION: HETEROCYCLIC SUBSTITUTED
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 36
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-10-671-242-36
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US-10-820-487-9
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LENGTH: 48
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ADDRESSEE: Fish &
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Sequence 12, Application US/10479472A

Sequence 12, Application US/10479472A

Sequence 12, Application Worsobsoll8581A1

GENERAL INFORMATION:

APPLICANT: DEL-FAVERO, JURGEN PETER LODE

APPLICANT: VAN BROEKGHOVEN, CHRISTINE

TITLE OF INVENTION: NOVEL BRAIN EXPRESSED GENE AND PROTEIN ASSOCIATED WITH

TITLE OF INVENTION: NOVEL BRAIN EXPRESSED

FILE REFERENCE: JAB-1711

CURRENT PELING DATE: 2003-12-01

PRIOR PILING DATE: 2003-06-06

PRIOR FILING DATE: 2002-06-06

PRIOR FILING DATE: 2001-06-11

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver: 3.2

SEQ ID NO 12

LENGTH: 36
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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US-10-479-472A-12
                                                                                                                                                                                                                                                                                                                              Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28.6; DB 21; Length 36;
Pred. No. 3.4e+03;
                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                         Score 28.6; DB 17;
Pred. No. 3.4e+03;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                      231 GAGGACGAGGAGGAGGAGGAGGAGGAAGAGGA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGGAAGAGGAGGAAGAAGAAGAAGAAGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
CURRENT APPLICATION NUMBER: US/10/418,182
CURRENT FILING DATE: 2003-04-16
PRIOR PILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 423
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 86
LENGTH: 36
                                                                                                                                                                                                                                               ; OTHER INFORMATION: oligonucleotide US-10-418-182-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30, Application US/09962055
Sequence 30, Application US/09962055
Patent No. US20020052033A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.6%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.6%;
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-962-055-30
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Sequence 30, Application US/09976740

Publication No. US20020194633A1

GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Lees, Annelal A.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: ALjona Annelal A.
APPLICANT: ALjona Annelal A.
APPLICANT: ALjona Annelal A.
APPLICANT: ALJONA AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATRENOSCIEROSIS
FILE REPERENCE: 10797-04001
CURRENT FILING PAFE: 2001-10-12
CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/979,608
PILING DATE: 2-NOV-1997
APPLICATION NUMBER: US 60/031,930
PILING DATE: 27-NOV-1996
ATTORING PIEL 27-NOV-1996
ATTORING PIEL 1 NFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPRONE 617/542-5070
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Indels
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                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPBRATURE SYSTEM: DOS
OPFRARE: FRSESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB 9; 1
Pred. No. 5.6e+03;
0; Mismatches 10
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PRIOR APPLICATION NUMBER: 09/616, 289
PRIOR PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979, 608
PRIOR PELING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048, 547
PRIOR FILING DATE: 1997-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1...45
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
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SOFTWARE: FastSEQ for Windows Version 4.0
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coding Sequence
                                                                                                                   ZIP: 02110-2804
UTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.2%;
Best Local Similarity 77.3%;
Matches 34; Conservative
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0; Gaps
                                                                                                                 Query Match 1.2%; Score 28; DB 9; Length 45; Best Local Similarity 77.3%; Pred. No. 5.6e+03; Matches 34; Conservative 0; Mismatches 10; Indels
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-976-740-30
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Search completed: August 4, 2005, 00:50:15 Job time : 1409 secs

score:

Sequence:

nucleic

Run on:

Scoring table:

Searched:

Database

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PAT 20-APR-2002
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BD056452 Novel low AB02058 Canis fam AXX48252 Sequence CQ003027 Sequence AX30654 Sequence AX934709 Sequence AX914709 Sequence AX55605 Sequence AX55605 Sequence AX55605 Sequence AX55605 Sequence AX55605 Sequence AX5605 Sequence GC073444 Sequence CC073444 Sequence BD274324 Identific BB274324 Identific BB274325 Identific BB274325 Identific BB274325 Identific
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1 (bases 1 to 48)

Crouzet, J., Scherman, D., Wils, P., Blanche, F. and Cameron, B. Purification of a triple helix formation with an immobilized oligonucleotide
Patent: US 6319672-A 34 20-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crouzet, J., Scherman, D., Wils, P., Blanche, F. and Cameron, B.
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Pred. No. 2e+04;
0; Mismatches 6; Indels
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synthetic construct
other sequences; artificial sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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Sequence 34 from Patent W00192511.
AX323399.1 GI:18094161
                                        AX248252
CQ003259
CQ003259
AX914709
AX912055
AX912055
AX914709
AX91403
AX91409
AX9109
AX9109
AX9109
CQ004509
AX200395
AX200395
AX103
AX9109
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/organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AR178317.1 GI:20219455
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1 Similarity 87.2%;
41; Conservative 0
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                                                                                                                                      Query Match
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AX323399
LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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VERSION
KEYWORDS
SOURCE
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VERSION
KEYWORDS
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AUTHORS
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AR178317
LOCUS
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      ORIGIN
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AR167590 Sequence
AR32338 Sequence
AK36852 Sequence
AR199544 Sequence
AR39544 Sequence
AR39533 Sequence
AR39533 Sequence
AR39538 Sequence
AR39538 Sequence
AR39538 Sequence
AR374690 Sequence
                                                                                                                                      3, 2005, 17:11:04; Search time 9527 Seconds (without alignments) 11392.850 Million cell updates/sec
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AX323399 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                            1839042
                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                    4708233 segs, 24227607955 residues
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                    nucleic search, using sw model
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AX323382
AX686852
AR199544
AR374696
AR409331
AX239593
BD056458
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AR409325
AX239587
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Gapop 10.0 , Gapext 1.0
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2240
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gb_sy:*
gb_un:*
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gb_in::;
gb_in::;
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gb_pt::;
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gb_r::;
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Match Length
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Result

Gaps

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PAT 20-APR-2002

JOURNAL

TITLE

FEATURES

ORIGIN

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1 (bases 1 to 50)
Crouzet, J., Scherman, D., Wils, P., Blanche, F. and Cameron, B. Purification of a triple helix formation with an immobilized oligonucleotide and 17 20-NOV-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crouzet, J., Scherman, D., Wils, P., Blanche, F. and Cameron, B. Purification of a triple helix formation with an immobilized oligonucleotide
Patent: WO 0192511-A 17 06-DEC-2001;
Aventis Pharma (FR)
Location/Qualifiers
                                                                                                              231 GAGGACGAGGAGGAAGAAGAGGAGGAGGAAGGAGGACGA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 50;
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                                                Length 50;
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                                             1.7%; Score 37.4; DB 6;
87.2%; Pred. No. 2e+04;
iive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..50
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.7%; Score 37.4; DB 6
ilarity 87.2%; Pred. No. 2e+04;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.7%; Score 37.4; DB 6
87.2%; Pred. No. 2e+04;
tive 0; Mismatches
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                                                                                                                                                                                                                          Sequence 17 from patent US 6319672.
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .50
/organism="unknown"
/wol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 from Patent WO0192511. AX323382
                                                                                                                                                                                                                                                                         AR178300.1 GI:20219438
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synthetic construct
                                                                                41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Conservative
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Best Local Similarity
Matches 41; Conserva'
                                                                                                                                                                                                                                                                                                                                         Unclassified.
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nes 41; Conserv
                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                         Unknown.
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ORGANISM
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VERSION
                                                                              Matches
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AUTHORS
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TITLE
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KEYWORDS
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AR178300
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AX323382
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1 (bases 1 to 50)

Crouzet, J., Scherman, D. and Wils, P.
Purification of a triple helix formation with an immobilized
oligonuclectide
Patent: US 6287762-A 17 11-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 50)
Crouzet,J., Scherman,D. and Wils,P.
PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN IMMOBILIZED
Purification of a triple helix formation with an immobilized
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                                                                                                                                                                             Score 37.4; DB 6; Lengturater No. 2e+04;
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                                                                                                            /mol_type="unassigned DNA"
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/note="synthetic oligonucleotide"
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Pred. No. 2e+04;
0; Mismatches 6;

    .48
    /organism="synthetic construct"

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Other publication AU 4178996 960703
Other publication FR 2728264 960621.
Location/Qualifiers
               oligonucleotide
Patent: WO 0192511-A 34 06-DEC-2001,
Aventis Pharma (FR)
Location/Qualifiers
                                                                                                                                                                                                                            0; Mismatches

    .50
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    /db_xref="taxon:32644"

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Sequence 17 from patent US 6287762.
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/organism="unknown"
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Best Local Similarity 87.2%;
Matches 41; Conservative
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Local Similarity 87.2%;
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DEFINITION ACCESSION VERSION

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SOURCE

AUTHORS TITLE

JOURNAL

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PAT 07-JAN-2002

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REFERENCE AUTHORS JOURNAL

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Homo sapiens (human)
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Unclassified.
Unclassified.
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                                                                                                                                                                Couzet, J., Scherman, D. and Wils, P.
Purification of a triple helix formation with an immobilized oligonucleotide
Patent: EP 128174-A 17 05-FEB-2003;
Aventis Pharma S.A. (FR)
Location/Qualifiers
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Lees.A.M., Lees.R.S., Law,S.W. and Arjona,A.A.
Low density lipoprotein binding proteins and their use diagnosing and treating atherosclerosis
Patent: US 6355451-A 36 12-MAR-2002;
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    .50
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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/mol_type="unassigned DNA"
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Sequence 36 from patent US 6605588.
AR374696
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AR199544
                                              Sequence 17 from Patent EP1281774.
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                                                                                                                unidentified
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Best Local Similarity
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Best Local Similarity
Matches 40; Conserva
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PAT 18-DEC-2003
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 48)
Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
Low density lipoprotein binding proteins and their use in
diagnosing and treating atherosclerosis
Patent: US 6632923-A 36 14-OCT-2003;
1 (bases 1 to 48)
Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density lipoprotein binding proteins and their use in
diagnosing and treating atherosclerosis
Patent: US 6605588-A 36 12-AUG-2003;
Location/Qualifiers
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1.6%; Score 35.2; DB 6; Length 48;
Best Local Similarity 83.3%; Pred. No. 4.9e+04;
Matches 40; Conservative 0; Mismatches 8; Indels
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/wol_type="genomic DNA"
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/mol_type="genomic DNA"
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AR409331.1 GI:40160119
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PAT 16-JAN-2004
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1 (bases 1 to 36)

Davies, K.E. and Theodosiou, A.

MURINE GUANINE NUCLEOTIDE EXCHANGE FACTOR - (MNGEF) AND HUMAN
HOMOLOGUES THEREOF
PETENT: WO 9823743-A 10 04-UNN-1998;
MEDICAL RES COUNCIL (GB); DAVIES KAY ELIZABETH (GB)
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Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0147944-A 1427 05-JUL-2001;
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Pred. No. 8.6e+05;
0; Mismatches 5; Indels
                                                                  Length 39;
                                                                                                                                                                                                                                                                                                                                  linear
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/db_xref="taxon:9606"
/note="Accession number cg43955901"
                                                                                                                                                                 232 AGGACGAGGAGGAAGAAGAGAGGAGGAGGAGGACG
                                                                                                                                                                                                             39 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
                                                                  Score 31; DB 6; I
Pred. No. 2.6e+05;
0; Mismatches 5;
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
1. .36
/mol_type="unassigned DNA"
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Sequence 10 from Patent WO9823743.
A91851
A91851.1 GI:6740735
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Location/Qualifiers
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CQ002787.1 GI:41009419
                                                             1.4%;
Best_Local Similarity 87.2%;
Matches 34; Conservative (
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Best Local Similarity 86.1%;
Matches 31; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequorea victoria
Sequorea victoria
Sequorea victoria
Butaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Butaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Butaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Bequoreidae; Aequorea.

I (bases 1 to 48)
Subsequoreidae; Jaw, S.W. and Arjona, A.A.
Subsequoreidae; Jaw, S.W. and Arjona, A.A.
Subsequoreidae; Jaw, S.W. and Arjona, A.A.
Butaryota; Lees, R.S.; Law, S.W. and Arjona, A.A.
Bostow Heart Foundation inc
Proposition of their use in diagnosing and treating atherosclerosis
Bostow Heart Foundation inc
PN JP 2001506983-A,16
PN 
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Schalling,M., Hudson,T.J. and Housman,D.E.
Direct detection of expanded nucleotide repeats in the human genome Patent: US 5695333.A 9 09-DEC-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                       BD056458 10 DNA linear PAT 27-AUG-2002 Novel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis,.
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                                            1.6%; Score 35.2; DB 6; Length 48; 83.3%; Pred. No. 4.9e+04;
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/organism="Aequorea victoria"
/mol type="genomic DNA"
/db_xref="taxon:6100"
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184408
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JP 2001506983-A/16.
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Search completed: August 4, 2005, 00:26:44 Job time : 9532 secs

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August 3, 2005, 17:10:58; Search time 1182 Seconds (without alignments) 11218.461 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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2240
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		Description	Abz00752 Human leu	Adg33274 Human DNA	Aas21106 (GGA)16 D	Aat32776 Homopurin	Aas19342 Plasmid X	Aah26508 Low densi	Aaf31000 Human NOG	Aaf30999 Human NOG	Abz22128 Polyanion	Abz22092 Polyanion	Aal28219 Human SNP	Aah26502 Low densi	Aai29843 Human sin	Aai64451 SSR motif	Aas13776 Simple se	Aal28459 Human SNP	Aal28691 Human SNP	Aas13779 Simple se	Adc56858 Micro gol	Adc56859 Micro gol
SUMMARIES		ΙD	ABZ00752	ADG33274	AAS21106	AAT32776	AAS19342	AAH26508	AAF31000	AAF30999	ABZ22128	ABZ22092	AAL28219	AAH26502	AAI29843	AAI64451	AAS13776	AAL28459	AAL28691	AAS13779	ADC56858	ADC56859
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	* 6	Match	2.2	2.5	1.7	1.7	1.7	1.6	1.5	1.5	1.4	1.4	1.3	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2
		Score	50	20	37.4	37.4	37.4	35.2	34	34	32.4	32.4	28.2	28	27.4	27.4	26.6	26.6	26.2	56	26	26
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Abz22048 Polyanion	Aav55838 Sequence	Aac26760 Human sec	Adj81490 Plant ret	Aav76464 Staphyloc			Abx04111 Oligonucl	Abz22047 Polyanion	Abz22086 Polyanion	Aat17027 Human mit	Humar	Aac64407 Human Nog	Rena	Renal	Adp17617 Renal cel	Renal	Adp17619 Renal cel	Renal	Adp17616 Renal cel	a	623 Renal	Renal	Adp17620 Renal cel	Adp17624 Renal cel	
ABZ22048	AAV55838	AAC26760	ADJ81490	AAV76464	ABZ59596	ABN81202	ABX04111	ABZ22047	ABZ22086	AAT17027	ABK94441	AAC64407	ADP17627	ADP17614	ADP17617	ADP17618	ADP17619	ADP17613	ADP17616	ADP17622	ADP17623	ADP17628	ADP17620	ADP17624	
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1.2	1.2	1.2	1.1	٦. ٦	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	
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c 21	22	c 23	24	52	26	7	c 28	29	30	c 31	32	c 33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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ABZ00752 standard; DNA; 50

RESULT 1

ABZ00752;

17; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe; New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides. Phillips J; Human leukocyte gene expression profiling probe SEQ ID NO 743. Prentice J, nuth J, Fry K, Matcuk G, Altman P, P) Woodward R, Quertermous T, Johnson F; 22-OCT-2001; 2001WO-US047856. 20-OCT-2000; 2000US-0241994P. 08-JUN-2001; 2001US-0296764P. (first entry) (BIOC-) BIOCARDIA INC. WPI; 2002-636525/68. WO200257414-A2. Wohlgemuth J, Homo sapiens. 09-JAN-2003 25-JUL-2002. Ľ, CCCCXSXXLLLXBXBXBXBXBXBXBXXXXXXXBXXBXXXXCXCCCCX

The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful

Claim 1; Page 348; Opp; English.

level of the differentially expressed diagnostic genes of the invention.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing or monitoring autoimmune and chronic inflammatory diseases, such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative colitis, psoriasis and asthma by detecting the expression level of one or
for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DNA probe used to monitor expression of diagnostic genes SeqID598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; ss; autoimmune; chronic inflammatory disease; SLE; systemic lupus erythematosis; rheumatoid arthritis; cholecystitis; Sjogren; disease; RESI syndrome; scleroderma; ankylosing spondylitis; ulcerative colitis; primary elecrosing cholangitis; appendicitis; diverticulitis; primary biliary sclerosis; probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nore genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG33274;
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8888888888888
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This invention comprises a method of purifying double-stranded DNA from a solution containing the double-stranded DNA mixed with other components, comprising passing the solution through a support comprising a covablently cupled oligonucleotide capable of forming a triple helix with the double-stranded DNA by hybridisation with a specific sequence present in the double-stranded DNA. The method is useful for purifying double-stranded DNA contained in a solution and mixed with other components. The new method enables DNA to be purified from complex mixtures comprising the runcleic acids, proteins, endotoxins, nucleases and the like. The supports may be readily recycled, and the DNAs obtained display improved properties to pharmaceutical safety. Further, the method entails only one step contrary to prior art. The present sequence represents a DNA sequence contained within the plasmid pXL2725. This sequence is used for purification of this plasmid using the method of the invention
                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purifying double-stranded (ds) DNA from a solution containing dsDNA and other components, comprises passing the solution through a support comprising a covalently coupled oligonucleotide able to form a triple
                                                                                         Gaps
                                                                                                                       2189
                                                                                         ..
                                                                                                                                                      20
                                                                                                                                           1 TGTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACTGT
                                                                                                                       2140 TGTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACTGT
                                                                                                                                                                                                                                                                                                                                                            ss; DNA purification; triple helix; plasmid purification.
                                                                                         0; Indels
                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cameron
                             Sequence 50 BP; 13 A; 6 C; 13 G; 18 T; 0 U; 0 Other;
                                                          DB 10;
0.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blanche F,
                                                                      Local Similarity 100.0%; Pred. No. 0.8 (es 50; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                              (GGA)16 DNA purification oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "GAA repeat type"
                                                          Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 7; Page 20; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_type= TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wils P,
                                                                                                                                                                                                                                    ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2001; 2001WO-US017122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000; 2000US-00580923.
                                                            2.28;
                                                                                                                                                                                                                                   AAS21106 standard; DNA; 48
                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ಡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AVET ) AVENTIS PHARMA SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scherman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                         ...48
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     helix with the dsDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-097772/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200192511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                               20-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crouzet J,
                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                  AAS21106;
                                                            Query Match
                                                                                           Matches
                                                                                                                                                                                                     RESULT 3
                                                                                                                                                                                                                       AAS21106
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ds; DNA purification; triple helix; plasmid purification; XL27256.

20-MAR-2002 (first entry)

Plasmid XL2725 sequence.

Location/Qualifiers

6. .50 /\*tag= a

repeat\_region

Key

Synthetic.

/\*tag= b /note= "GGA repeat type"

25-MAY-2001; 2001WO-US017122 26-MAY-2000; 2000US-00580923

WO200192511-A2

06-DEC-2001.

(AVET ) AVENTIS PHARMA SA

Crouzet J, Scherman D, WPI; 2002-097772/13.

/rpt\_type= TANDEM 6. .8 /\*tag= b

repeat\_unit

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Double-stranded (ds) DNA can be purified from complex mixtures of nucleic acids, proteins, endotoxins, nucleases, etc. by passing the mixture over a support to which an oligonuclecide is covalently attached; the oligonuclectide is able to form a triple helix by hybridisation with a specific sequence present in the dsDNA. The present sequence is a preferred homopurine target for triplex formation with a single-stranded oligonuclectide. The target sequence may be present naturally, e.g. in a plasmid origin of replication, or can be introduced artificially. The method is particularly suited to purification of plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purificn. of double stranded DNA by triple helix formation - comprises hybridising immobilised oligo-nucleotide to specific sequence in target
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triple helix, triplex formation, Hoogsteen base pairing; plasmid; purification; double-stranded DNA; homopyrimidine; polypurine; ss
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                                                                                                                                        231 GAGGACGAGGAGGAGGAGGAGGAGGAGGAGGACGAGGACGA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37.4; DB 6; Length 48; Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.7%; Score 37.4; DB 2; Length 50;
Best Local Similarity 87.2%; Pred. No. 3.4e+02;
Matches 41; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                    Homopurine target for triple helix-forming oligonucleotide.
                                                                                           6; Indels
Sequence 48 BP; 16 A; 0 C; 32 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 50 BP; 17 A; 0 C; 33 G; 0 T; 0 U; 0 Other;
                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scherman D, Wils P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 25; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHON ) RHONE POULENC RORER SA.
                                                                                                                                                                                                                                                                                                         AAT32776 standard; DNA; 50 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-FR001468.
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                                            Query Match
1.7%;
Best Local Similarity 87.2%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-300660/30.
                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9618744-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crouzet J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                     AAT32776;
                                                                                                                                                                                                                                                          RESULT 4

AAT32776

AAT327776

AAT327776

AAT327776

AAT
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Purifying double-stranded (ds) DNA from a solution containing dsDNA and other components, comprises passing the solution through a support comprising a covalently coupled oligonucleotide able to form a triple helix with the dsDNA.

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Cameron

Wils P, Blanche F,

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This invention comprises a method of purifying double-stranded DNA from a solution containing the double-stranded DNA mixed with other components, comprising passing the solution through a support comprising a covalently coupled oligonucleotide capable of forming a triple helix with the double-stranded DNA by hybridisation with a specific sequence present in the cuble-stranded DNA the method is useful for purifying double-stranded DNA contained, rapid and mixed with other components. The new method is a simple, rapid and effective method for DNA purification, and makes it possible to obtain especially high purities with high yields. The method enables DNA to be purified from complex mixtures comprising other nucleic acids, proteins, endotoxins, nucleases and the like. The supports may be readily recycled, and the DNAs obtained display improved step contrary to prior art. The present sequence represents the sequence of the plasmid XL2725 verified upon sequencing, this sequence differs from the expected sequence (GGA)17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.7%; Score 37.4; DB 6; Length 50; 37.2%; Pred. No. 3.4e+02; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 50 BP; 17 A; 0 C; 33 G; 0 T; 0 U; 0 Other;
Example 7.1; Page 20; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH26508 standard; DNA; 48 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 87.2%;
nes 41; Conservative
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Matches
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AAH26508
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AAS19342 standard; DNA; 50

AAS19342

RESULT 5
AAS19342
ID AAS1
XX
AC AAS1

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Michalovich D, Prinjha R;
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                                                                                                                                                                                                                                                                                                                        The present sequence is that of a polynucleotide encoding a fragment of novel low density lipoprotein binding proteins (LBPS) of the invention (see AAB82797-820). LBPS are capable of binding to native and methylated low density lipoproteins (LDLS). Isolated polynucleotides encoding novel LBPs and their fragments are claimed, as well as expression vectors, calls and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for reating a cell thaving an abnormality in structure or metabolism of LBP are also claimed, as are pharmaccutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOGO-A; human, chromosome 2p21, neuropathy, spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease; neuromuscular disorder; psychiatric disorder; developmental disorder; neuropuscular disorder; neuroperotective; nootropic; neuroleptic; antiparkinsonian; cerebroprotective; neuroleptic; diagnosis; therapy; PCR primer; ss.
                      Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine; ss.
                                                                                                                                                                                                                                                                New isolated low density lipoprotein binding polypeptide for treating diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 GACGAGGAGGAAGAAGAGGAGGAGGAAGAGGAGGAGGACGAAGAC 281
Low density lipoprotein binding protein (LBP) polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.6%; Score 35.2; DB 5; Length 48; 33.3%; Pred. No. 9.7e+02; ve. 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 48 BP; 17 A; 7 C; 24 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human NOGO-A cDNA antisense PCR primer.
                                                                                                                                                                                                                   Law SW, Arjona AA;
                                                                                                                                                                                                                                                                                                   Disclosure; Page 10; 143pp; English
                                                                                                                                                                                           BOST-) BOSTON HEART FOUND INC
                                                                                                                                                       02-MAR-2000; 2000US-00517849.
14-JUL-2000; 2000US-00616289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF31000 standard; DNA; 42 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-NOV-2000; 2000WO-GB004345.
                                                                                                                                 28-FEB-2001; 2001WO-US006356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40; Conservative
                                                                                                                                                                                                                                        WPI; 2001-565505/63
                                                                                                                                                                                                                   Lees AM, Lees RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                 WO200164874-A2.
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                                                                                                         07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF31000;
                                                           Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF31000/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
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The present sequence is that of an antisense primer designed for the PCR amplification of full-length human cDNA (see AAF90324) coding for NOGO-A (see AAB8249). Spinal cord cDNA was used stemplate. The invention relates to a novel splice variant, NOGO-C (see AAF90323), of the human NOGO gene. It provides NOGO-C polypeptides and polymucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polymucleotides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's discrders and Parkinson's disease, neuromuscular disorders, methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and diagnostic assays for detecting diseases associated with inappropriate NOGO-C activity or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease; neuromuscular disorder; psychiatric disorder; developmental disorder; neuropuscective; noctropic; neuroleptic; antiparkinsonian; cerebroprotective; neuroleptic; diagnosis; therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                   New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 4; Length 42;
Pred. No. 1.6e+03;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1246 GCAAAGCTGAATGAAAACGCCCAAAATAATTAGTAGGAGTTC 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 GCAAAGCTGAATGAAAACGCCCAAAATAATTAGTCTAGATTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42 BP; 9 A; 7 C; 8 G; 18 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 20; 25pp; English.
                                                                                                           (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
15-NOV-1999; 99GB-00026995.
24-JAN-2000; 2000GB-00001550.
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24-JAN-2000; 2000GB-00001550.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 88.1 les 37; Conservative
                                                                                                                                                                              Prinjha
                                                                                                                                                                                                                                                    WPI; 2001-343822/36.
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                                                                                                                                                                              Michalovich D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUL-2001
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Polyanionic polymer; bioactivity; water solubility; ss.
                                                                                                                                                                         Sequence 43 BP; 8 A; 14 C; 13 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                       Polyanionic polymer related oligonucleotide #82.
                                                                                                                                                                                                                 132 CCAGCCATGGAAGACCTGGACCAGTCTCCTCTGG 165
                                                                                                                                                                                                                         10 CCAGCCATGGAAGACCTGGACCAGTCTCCTCTGG 43
                                              Example 1; Page 20; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 7; Fig 8; 74pp; English.
                                                                                                                                                                                                                                                                ABZ22128 standard; DNA; 42 BP
                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2002; 2002WO-US008614.
                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001; 2001US-0277705P
                                                                                                                                                                                                                                                                                           11-MAR-2003 (first entry)
                                                                                                                                                                                             Best Local Similarity 100.
Matches 34; Conservative
       WPI; 2001-343822/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-058367/05.
                                                                                                                                                                                                                                                                                                                                                                                                       (LEUN/) LEUNG D W.
                                                                                                                                                                                                                                                                                                                                                 WO200277036-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                            Waggoner DW;
                                                                                                                                                                                                                                                                                                                                                               03-OCT-2002
                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                     ĎW,
                                                                                                                                                                                                                                                                              ABZ22128;
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product
                                                                                                                                                            levels
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Lofquist A, Pietz GE,

Bergman PA,

; 0 1.7e+03;

1.5%; Score 34; DB 100.0%; Pred. No. 1.7 :ive 0; Mismatches

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product tolmed by 1990 the product of the product tolmed by 1990 the product of the protein product (P) of EV where (P) is PP and at least 80% of PP is a protein product (P) of EV where (P) is PP and at least 80% of PP is a caproximately of the same molecular weight. Also described: (1) a recombinant fusion protein (1) comprising a polyanionic polymerial and polyanionic polymer (II) comprising a polyanionic polymer and polyanionic polymer is polyanionic polymer and leukine, where the polyanionic polymer is polyalutamic acid or polyaspartic acid; (3) a vector (III) comprising a cassette which comprises a nucleotide sequence encoding a polyanionic polymer and at least one other nucleotide sequence, where the polyanionic polymer is polyglutamic acid or polyaspartic acid; (4) production of (I); (5) a cell (IV) comprising (III) or a vector that is larger than 10 kDa; and (6) a recombinantly-produced polyanionic polymer (V) that is of any molecular encodes a polyanionic polymer (V) that is of any molecular encodes a polyanionic polymer (V) that is of any molecular a larger than 10 kD, and is conjugated to another protein. (I) is useful for treating a disease or ailment in an individual by administering (I) to the individual. (I) is also useful for delivering an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              effective amount of a pharmaceutically active agent, a therapeutic protein or a drug to a patient in need of it, or for diagnostic and testing or research purposes. ABZ22045 to ABZ22131 and ABP56374 to ABP56400 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing monodispersed preparation of polyanionic polymer for therapy, by expressing vector comprising ligation product of oligonucleotides encoding glutamate/aspartate residues in host cell and isolating the
monodispersed preparation of a polyanionic polymer (PP) larger than 10
                      kD. (M) involves inserting into an expression vector (BV) a ligation product formed by ligating together oligonucleotides that encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4%; Score 32.4; DB 10; Length 42; B5.7%; Pred. No. 3.5e+03; ive 0; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tompkins CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 GAGGACGAGGAAGAAGAGAGGAGGAGGAAGAGAGGACGAG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polyanionic polymer; bioactivity; water solubility; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 42 BP; 22 A; 0 C; 20 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polyanionic polymer related oligonucleotide #46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 5; 74pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LEUN/) LEUNG D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200277036-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABZ22092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                             The present sequence is that of a sense primer designed for the PCR amplification of full-length human cDNA (see AAF90324) coding for NOGO-A (see AAB82349). Spinal cord cDNA was used as template. The invention relates to a novel splice variant, NOGO-C (see AAF90323), of the human NOGO gene. It provides NOGO-C polypeptides and polymucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polymucleotides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychlatric disorders and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and diagnostic assays for
                                                                      New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing monodispersed preparation of polyanionic polymer for therapy, by expressing vector comprising ligation product of oligonucleotides encoding glutamate/aspartate residues in host cell and isolating the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detecting diseases associated with inappropriate NOGO-C activity or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Length 43;
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The present invention describes a method (M) for producing a monodispersed preparation of a polyanionic polymer (PP) larger than 10 kD. (M) involves inserting into an expression vector (EV) a ligation product (P) of EV, where (P) is PP and at least 80% of PP is glutamate/aspartate residues, expressing EV in a host cell, and isolating approximately of the same molecular weight. Also described: (1) a captoximately of the same molecular weight. Also described: (1) a contract polypeptide at either one end or at both ends of it; (2) a colther polypeptide at either one end or at both ends of it; (2) a colther polypeptide at either one end or at both ends of it; (2) a colther polypeptide at either comprising a polyanionic polymer and contract polymer (II) conjugate comprising a cassette which comprises a nucleotide sequence encoding a polyanionic polymer and at least one other nucleotide sequence, where the polyanionic polymer is polyanionic polyaner is comprised a polyanionic polymer (W) that is of any molecular eccomprised a polyanionic polymer (W) that is of any molecular weight or is larger than 10 kD, and is conjugated to another protein. (I) is useful for treating a disease or allment in an individual by administering (I) to the individual. (I) is also useful for delivering an effective amount of a pharmaceutically active agent, a therapeutic protein or a drug to a patient in need of it, or for diagnostic and a public of the individual. (I) is also useful for delivering and the protein or a drug to a patient in need of it, or for diagnostic and the public of the individual of the protein or a drug to a patient in the encodes and the protein or a drug to a patient in need of it, or for diagnostic and the public of the individual in the public of the public of the public of the individual in the public of the individual in the public of the public o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP56400 represent sequences used in the exemplification of the present
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                    88888888888888888888888888888888
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Sequence 42 BP; 22 A; 0 C; 20 G; 0 T; 0 U; 0 Other;

Gaps ö DB 10; Length 42; 6; Indels Score 32.4; DB 10 Pred. No. 3.5e+03, 0; Mismatches 1.4%; Matches 36; Conservative Query Match Best Local Similarity

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1 GAAGAGGAAGGAAGAAGAAGAAGAAGAAGAAGAG 42

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AAL28219 standard; DNA; 49 (first entry) 24-JAN-2002 AAL28219; RESULT 11 AAL28219/ 

BP

Human SNP oligonucleotide #1427.

Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopictin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytoking factor; interleukin; G-protein coupled receptor; thioesterase; intlammation; multifactorial disease; autoimmune disease; infection; nervous system disease; se.

Homo sapiens

WO200147944-A2.

05-JUL-2001.

28-DEC-2000; 2000WO-US035498.

99US-0173419P 27-DEC-2000; 2000US-00173419. 28-DEC-1999;

(CURA-) CURAGEN CORP.

Shimkets RA,

WPI; 2001-465210/50.

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Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
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Claim 1; Page 1788; 4143pp; English

The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, instones, kinases, colony stimulating factors, complement related proteins coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides of the prevention, diagnosis and treatment of diseases uch nistones that may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune consistency of the may be prevented, diagnosed and/or treated include systemic lugues exptremations and Grave's diseases, inflammation, cancer (e.g. cancers of the harder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms

Sequence 49 BP; 8 A; 4 C; 3 G; 34 T; 0 U; 0 Other;

Gaps ö DB 4; Length 49; 13; Indels Score 28.2; DB 4; Pred. No. 2.8e+04; 0; Mismatches Query Match
1.3%;
Best Local Similarity 73.5%;
Matches 36; Conservative

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AAH26502

AAH26502 standard; DNA; 45

12-NOV-2001 (first entry)

Low density lipoprotein binding protein (LBP) polynucleotide.

Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine; ss.

Mammalia.

WO200164874-A2.

07-SEP-2001.

28-FEB-2001; 2001WO-US006356.

02-MAR-2000; 2000US-00517849. 14-JUL-2000; 2000US-00616289.

(BOST-) BOSTON HEART FOUND INC

Law SW, Arjona AA; Lees RS, Lees AM,

WPI; 2001-565505/63

New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.

Disclosure; Page 9; 143pp; English.

The present sequence is that of a polynucleotide encoding a fragment of novel low density lipoprotein binding proteins (LBPs) of the invention (see AAB82797-820). LBPs are capable of binding to native and methylated The present novel low de

Revised record issued on 04-NOV-2004 : Correction to Feature Table Key

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype.
low density lipoproteins (LDLs). Isolated polynucleotides encoding novel LBPs and their fragments are claimed, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are also claimed, as are pharmaceutical compositions comprising an LBP polypeptide or
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; resequence, genotype; disease; forensic; patexnity testing; single nucleotide polymorphism; SNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/standard_name= "single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 GAGGAGGAAGAAGAGGAGGAGGAGGAGGACGACGACGAGGA 280
                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 5; Length 45; Pred. No. 3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGAGGAAGAAGATGATGAAGATGAAGATGAAGAAGATGA 44
                                                                                                                                                                                                                                                                                                              Sequence 45 BP; 22 A; 0 C; 16 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human single nucleotide polymorphism (SNP)
                                                                                                                                                                                                                                            nucleic acid, and vaccine compositions
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                                                                                                                                                                                                                                                                                                                                                                           1.2%;
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2000US-0206129P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI29843 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.35
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22-MAY-2000;
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18-OCT-2001
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variation
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AAC AA12
AAC AA12
AAC AA12
BAC AA12
BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 mucleotide core element which is trandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel simple sequence repeats in clover species useful for selection genes in legume breeding, for profiling legume species varieties and testing the purity of legume seed batches.
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                  Simple Sequence Repeat, SSR, clover, microsatellite, genome mapping, trait mapping, marker-assisted selection, gene selection, legume, DNA profiling, breeding, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.2%; Score 27.4; DB 4; Length 45; Best Local Similarity 75.6%; Pred. No. 4e+04; Matches 34; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 ACGAGGAGGAAGAAGAGGAGGAAGAGAGGAGGACGAGGACGAAG 279
                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                               Sequence 31 BP; 13 A; 1 C; 16 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45 BP; 0 A; 15 C; 0 G; 30 T; 0 U; 0 Other;
                                                             Score 27.4; DB 4;
Pred. No. 3.5e+04;
0; Mismatches 1;
                                                                                                                            268
                                                                                                                                                           GAGGAAGAAGAGGAGGACGAGGAGGA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AGRI-) AGRIC VICTORIA SERVICES PTY LTD
                                                                                                                            240 GAGGAAGAGAGGAGGAGGAAGAGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 35; 52pp; English.
                                                              1.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JAN-2001; 2001NZ-00509194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-2000; 2000AU-00006520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99AU-00004907
                                                                                                                                                                                                                                       AA164451 standard; DNA; 45
                                                      Query Match
Best Local Similarity 96.6
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koelliker R, Forster JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-431058/46.
                                                                                                                                                                                                                                                                                                                                    SSR motif #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-DEC-1999;
                                                                                                                                                                                                                                                                                                      23-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NZ509194-A.
                                                                                                                                                                                                                                                                       AAI64451;
                                                                                                                                                         N
                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                            AAI64451,
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BP.

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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence crepeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer 2-6 nucleotides in length. Also included are a nucleic acid primer cuitable for amplifying an SSR, identifying (M1) an SSR by preparing a Library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breading by identifying an SSR that is closely associated with the gene such that the SSR and the gene are method for DNA profiling grass or cereal species varieties by assessing and resting the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for grass or cereal seed batches, and for DNA profiling to establish the grass or cereal secd batches, and for DNA profiling to establish the grass or describent ity and/or stability of a cultivar. The present sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                     Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 42 BP; 28 A; 0 C; 14 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                               UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO.
UNIV ADELADIA
INT MAIZE & WHEAT IMPROVEMENT CENT.
                                                                                                                 Simple sequence repeat, SSR, #47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 53; 72pp; English.
                                                                                                                                                                                                                                                                                                                                   03-JAN-2001; 2001NZ-00509193.
                                                                                                                                                                                                                                                                                                                                                                      24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
AAS13776 standard; DNA; 42
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Forster JW, Jones ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-512563/56.
                                                                          08-MAY-2002
                                                                                                                                                                                                                                                                                             25-MAY-2001
                                                                                                                                                                                                                                                      NZ509193-A.
                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       varieties
                                    AAS13776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ITMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                SAUS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYSC-)
(VICT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UYAD-)
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Gaps

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1.2%; Score 26.6; DB 4; Length 42; 78.0%; Pred. No. 5.8e+04; tive 0; Mismatches 9; Indels

240 GAGGAAGAAGAGGAGGAAGAAGAGGACGACGACGAAGA 280 

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32; Conservative

Search completed: August 3, 2005, 21:47:49 Job time : 1186 secs